TUESDAY POSTERS

INSTRUMENTATION: FTMS, 004 - 020

TP 004 **Ion Accumulation and Storage in a Radiofrequency Octopole Ion Trap**; Maria Van Agthoven[1]; Steve Beu[2]; Greg T. Blakney[1]; John Paul Quinn[1]; Chris Hendrickson[1]; Alan G. Marshall[1]; *[1]National High Magnetic Fields Laboratory, Tallahassee, FL; [2]S C Beu Consulting, Austin, TX*

TP 005 **A Compact FT-ICR Mass Spectrometer with a Field-Emission Cathode for Metabolomics and Proteomics Applications**; Andrey N. Vilkov; Chaminda M. Gamage; Vladimir M. Doroshenko; *MassTech Inc., Columbia, MD*

TP 006 **Performance Enhancement for a Hybrid 1 T Permanent Magnet ESI-FTICR Mass Spectrometer using Multiple Frequency Detection**; Pavel N. Sagulenko[1]; Dmitry A. Tolmachev[1]; Andrey Vilkov[2]; Vladimir M. Doroshenko[2]; Mikhail V. Gorshkov[1]; *[1]Institute of Energy Problems of Chemical Physics R, Moscow, Russian Federation; [2]Masstech, Inc., Columbia, MD*

TP 007 **Simulation Study on Stacked Ring Ion Guide for FT-ICR MS to Reduce Time of Flight Discrimination**; Sunghwan Kim; Myoung-choul Choi; Seungyong Kim; Hyun Sik Kim; Young Hwan Kim; Jong Shin Yoo; *Korea Basic Science Institute, Ochang-myun, Korea*

TP 008 **Broadband Phase Correction of Complex FT-ICR Mass Spectra**; Feng Xian [5]; Chris Hendrickson[1]; Greg T. Blakney[2]; Steve Beu[3]; Alan G. Marshall[4]; *[1]National High Magnetic Field Laboratory, Tallahassee, FL; [2]National Ft-icr Program At Nhmfl, Tallahassee, FL; [3]S C Beu Consulting, Austin, TX; [4]Ion Cyclotron Resonance Prog, Tallahassee, FL; [5]Florida State University, Tallahassee, FL*

TP 009 **Subtle Behaviors in an Electrically Compensated Cylindrical ICR Cell**; Adam Brustkern; Don L. Rempel; Michael L. Gross; *Washington University, St. Louis, MO*

TP 010 **Changes in Ion Kinetic Energy Distribution during Transfer through a Multipole Ion Guide in a Strong Magnetic Field Gradient**; Steve Beu[1]; Chris Hendrickson[2]; Alan G. Marshall[2]; *[1]S C Beu Consulting, Austin, TX; [2]National High Magnetic Field Laboratory, Tallahassee, FL*

TP 011 **Application of a "Lock Mass" on an LTQ Orbitrap to Maintain Accurate Mass Assignments throughout Large Biomarker Discovery Studies;** Ekaterina G. Deyanova[1]; Wolfgang Metelmann-strupat[2]; Emile Deleeuw[2]; Matthew Mazur[1]; Nathan Yates[1]; Kai Zhou[1]; Robert Settlage[1]; Ronald Hendrickson[1]; *[1]Merck Research Laboratories, Rahway, NJ; [2]Thermo Electron (Bremen) Gmbh, Bremen, Germany*

TP 012 **Improving the Performance of a GC-FT-ICR MS using an External EI/CI Ion Source**; Jan E. Szulejko; Behrooz Zekavat; Touradj Solouki; *University of Maine, Orono, ME*

TP 013 **Trapping Ring Electrode Cell (TREC): A Novel ICR Cell for Ultra-High Sensitivity, Resolution, and Mass Measurement Accuracy**; Chad R. Weisbrod; Nathan K. Kaiser; Gunnar E. Skulason; James E. Bruce; *Washington State University, Pullman, WA*

TP 014 **Synchronization of Ion Activation and Electron Capture Dissociation with Ion Magnetron Motion in an FT-ICR Mass Spectrometer**; Victor A. Mikhailov; Helen Cooper; *University of Birmingham, Birmingham, UK*

TP 015 **Experimental Evidence of Ion Cyclotron Resonance Frequency Modulations Induced by Inhomogeneities of the Trapping Electric Field**; Konstantin Aizikov[1]; Nadezda P. Sargaeva[2]; Jason J Cournoyer[3]; Cheng Lin[2]; Peter B. O'connor[2]; *[1]BUSM Mass Spectrometry, Boston, MA; [2]Boston University, Boston, MA; [3]Boston University Medical School, Boston, MA*

TP 016 **Performance of a High-Field Orbitrap Mass Analyzer**; Alexander Makarov; Eduard Denisov; Oliver Lange; Wilko Balschun; Jens Griep-raming; *Thermo Fisher Scientific (Bremen) GmbH, Bremen, Germany*

TP 017 **A Wire-Ion-Guide ICR Cell for Low-Magnetic-Field FT-ICR MS**; Chaminda M. Gamage[1]; Andrey N. Vilkov[1]; Kent J. Gillig[2]; David H. Russell[2]; Vladimir M. Doroshenko[1]; *[1]MassTech, Inc., Columbia, MD; [2]Texas A&M University, College Station, TX*

TP 018 **New Hardware for Ultrahigh Resolution and/or Data-Dependent SWIFT Ion Isolation in an FT-ICR Mass Spectrometer**; Greg T. Blakney; Chris Hendrickson; John Paul Quinn; Alan G. Marshall; *National ICR Program at NHMFL, Tallahassee, FL*

TP 019 **A Representation of the Possible Frequency Surfaces for an FTMS Cylindrical Compensable Trap that Facilitates Investigation of Trap Operation**; Don L. Rempel; Adam Brustkern; Michael L. Gross; *Washington University, St Louis, MO*

TP 020 **External Calibration Strategies for High Magnetic Field FT-ICR MS Coupled with Automatic Gain Control**; Tanner M. Schaub[1]; Chris Hendrickson[2]; Alan G. Marshall[3]; *[1]National High Magnetic Field Laboratory, Tallahassee, FL; [2]Ion Cyclotron Resonance Prog, Tallahassee, FL; [3]Dept. of Chem. and Biochem., Florida State Univ., Tallahassee, FL*

DIRECT IONIZATION 2, 021 - 036

TP 021 **A Comparative Study of DESI and DART on a Mobile Lab Atmospheric Pressure Ionization Ion Trap MS**; Michael Roth; Mitch Wells; *Griffin Analytical Technologies, West Lafayette, IN*

TP 022 **Profiling Intact Untreated Bacteria *in vivo* using Desorption Electrospray Ionization (DESI)**; Isabella Zhang; Nari Talaty; Anthony Costa; W. Andy Tao; R. Graham Cooks; *Purdue University, West Lafayette, IN*

TP 023 **Heat Transfer and Fluid Dynamic Simulations of a DART-type Ambient Mass Spectrometry Ion Source;** Facundo Fernandez; Glenn A Harris; *Georgia Institute of Technology, Atlanta, GA*

TP 024 **Development of Automated Protein Identification by nLC EWOD DESI FT-ICR ECD MS-MS**; Adam A. Stokes[1]; Chris Galloway[2]; Yifan Li[1]; William Parkes[1]; Dryden David[1]; Anthony J. Walton[1]; Pat Langridge-Smith[1]; C. Logan Mackay[1]; *[1]The University of Edinburgh, Edinburgh, UK; [2]Bruker Daltonics, Coventry, UK*

TP 025 **Second Generation DESI Ion Source for FTICR**; Vladimir Havlicek[1]; Gary Kruppa[2]; Karel Lemr[3]; Petr Novak[1]; Marian Hajduch[1]; Vaclav Kobliha[1]; Karel Sefcik[1]; Zoltan Takats[4]; *[1]Institute of Microbiology, Prague 4, Czech Republic; [2]Bruker Daltonics Inc., New York, NY; [3]Palacky University, Olomouc, Czech Republic; [4]Semmelweis University, Budapest, Hungary*

TP 026 **Enabling More Efficient Ion Collection in Surface Ionization Experiments**; Elizabeth A. Crawford; Brian D. Musselman; Joseph Tice; *IonSense, Inc., Saugus, MA*

TUESDAY POSTERS

TP 027 **HPTLC/DESI-MS Imaging of Tryptic Protein Digests Separated in Two Dimensions**; Sofie P. Pasilis [1]; Vilmos Kertesz[1]; Gary J. Van Berkel[1]; Michael Schulz[2]; Susanne Schorcht[2]; *[1]Oak Ridge National Laboratory, Oak Ridge , TN; [2]Merck KGaA, Darmstadt, Germany*

TP 028 **Enhanced Performance of a Liquid Microjunction Surface Sampling Probe using ESI and APCI**; Gary J. Van Berkel [1]; Vilmos Kertesz[1]; Bradley Schneider[2]; Thomas Covey[2]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN; [2]Mds Sciex, Concord, ON*

TP 029 **Laser-Induced Acoustic Desorption/Electrospray Ionization Mass Spectrometry for Directly Characterizing the Biological Compounds in Liquids under Ambient Conditions**; Sy-Chyi Cheng; Jentaie Shiea; *National Sun Yat-Sen Univ., Kaohsiung, TAIWAN*

TP 030 **Utility of Reactions in the Source of a Helium Metastable-Beam Open-Air-Ion-Source Mass Spectrometer**; Matthew Curtis; Patrick R. Jones; O. David Sparkman; *University of the Pacific, Stockton, CA*

TP 031 **Developing reliable measurements in DESI**; Felicia Green[1]; Peter Stokes[2]; Gavin O'Connor[2]; Ian Gilmore[1]; *[1]National Physical Laboratory, Teddington, UK; [2]Lgc Limited, Teddington, UK*

TP 032 **DESI-MS Direct Analysis of Anabolic Steroids Separated with Pressurized Planar Electrochromatography (PPEC)**; Dariusz J. Janecki[1]; Scott D. Woodward[2]; Justin M. Wiseman[1]; David Nurok[2]; *[1]Prosolia Inc., Indianapolis, IN; [2]Department of Chemistry and Chemical Biology IUPUI, Indianapolis, IN*

TP 033 **Analysis of Continuous-Flow Liquid Samples by Desorption Electrospray Ionization-Mass Spectrometry (DESI-MS)**; Zhixin Jessie Miao; Hao Chen; *Ohio University, Athens, OH*

TP 034 **Factors Affecting Signal Levels in HPTLC/DESI-MS of Dipeptides and Tryptic Peptides**; Arron B. Wolk[1]; Sofie P. Pasilis[2]; Vilmos Kertesz[2]; Gary J. Van Berkel[2]; *[1]Colorado College, Colorado Springs, CO; [2]Oak Ridge National Laboratory, Oak Ridge , TN*

TP 035 **Comparison of Drug Distribution Images from Thin Tissue Sections Obtained using Desorption Electrospray Ionization Tandem Mass Spectrometry and Whole-Body Autoradiography**; Vilmos Kertesz[1]; Gary J. Van Berkel[1]; Marissa Vavrek[2]; Kenneth A. Koeplinger[2]; Bradley B. Schneider[3]; Thomas R. Covey[3]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN; [2]Merck Research Laboratories, West Point, PA; [3]MDS Sciex, Concord, ON*

TP 036 **Transmission Mode Sample Introduction for High Throughput Desorption Electrospray Ionization**; Joe Chipuk; Jennifer Brodbelt; *University of Texas, Austin, TX*

MALDI SAMPLE PREPARATION, 037 - 066

TP 037 **Solvent-Free MALDI TOF/TOF Analysis of Metal Complexes**; John F. Berry[1]; Shu Yao[1]; Michael Nippe[1]; Sergei Dikler[2]; Martha M. Vestling[1]; *[1]University of Wisconsin, Madison, WI; [2]Bruker Daltonics, Inc., Billerica, MA*

TP 038 **Development of Copolymer Planar Microarray Chips (pMALDI) for Mass Spectrometry Based Proteomic and Genomic Analysis**; Alexandr Muck; Alfredo J. Ibanez; Vincentius A. Halim; Ales Svatos; *Max Planck Institute for Chemical Ecology, Jena, Germany*

TP 039 **Protein Identification by Rapid Acid Hydrolysis using MALDI Matrices: Comparison to Formic Acid Proteolysis**; Elizabeth R. Remily; Hayley Dirscherl; Nupam Mahajan; John Koomen; *H. Lee Moffitt Cancer Center, Tampa, FL*

TP 040 **DNA Isolation and Desalting Directly on Stainless Steel MALDI Plate for MS Analysis**; Igor P. Smirnov; Galina E. Pozmogova; Vadim M. Govorun; *Institute of Physico-Chemical Medicine, Moscow, Russian Federation*

TP 041 **Isolation and Identification of Sulfated Oligosaccharides by MALDI-MS**; Ming Lei; *Indiana University, Bloomington, IN*

TP 042 **CHCA or DHB? Matrix Selection and Optimization from a Facility Point of View**; Cunjie Zhang; Haixia Zhang; David W. Litchfield; Ken Yeung; Kristina Jurcic; *University of Western Ontario, London, ON, Canada*

TP 043 **Accurate Mass Measurement of Negative Radical Ions by MALDI-TOFMS: Application to Functionalized Fullerenes**; Shao Zhecheng; Mark F Wyatt; Bridget Stein; Gareth Brenton; *Swansea University, Swansea, UK*

TP 044 **Surface-Assisted Laser Desorption/Ionization Mass Spectrometry (SALDI-MS) of Low Molecular Weight Organic Compounds using ZnO Nanoparticles**; Ryuichi Arakawa[1]; Hideya Kawasaki[1]; Takehiro Watanabe[1]; Tetsu Yonezawa[2]; *[1]Kansai University, Osaka, Japan; [2]The University of Tokyo, Tokyo, Japan*

TP 045 **Comparison of Solvent-Free and Solvent-Based Sample Preparations for the Analysis of Polyethylene Glycols using Dihydroxybenzoic Acid Isomers in MALDI-MS;** Aera Lee[1]; Hyo-Jik Yang[1]; Jeongkwon Kim[1]; Yangsun Kim[2]; *[1]Chungnam National University, Daejeon, South Korea; [2]Hudson Surface Technology, Newark, NJ*

TP 046 **Atmospheric Pressure Laser Desorption Ionization using Colloidial Graphite and Silver Colloid for the Determination of Plant Metabolites**; David Perdian; Gregg Schieffer; R. Sam Houk; *Iowa State University, Ames, IA*

TP 047 **High-Sensitivity Liquid UV-MALDI-MS Analysis**; Mark W Towers; Rainer Cramer; *The University of Reading, Reading, UK*

TP 048 **The Comparison of Pencil Assisted Laser Desorption/Ionisation (PALDI) and MALDI for Quantitative Analysis**; Julie Herniman; G. John Langley; *University of Southampton, Southampton, UK*

TP 049 **Increased Sensitivity for Neuropeptide Analysis by Atmospheric Pressure Matrix-Assisted Laser Desorption/Ionization with Dynamic On-Chip Purification and Preconcentration/Focusing Targets;** Arti Navare[1]; Marcela Nouzova[3]; Salvador Hernandez[4]; Fernando Noriega[3]; Facundo Fernandez[2]; *[1]Georgia Tech, Atlanta, GA; [2]Georgia Institute of Technology, Atlanta, GA; [3]Florida International University, Miami, FL; [4]Instituto Nacional de Salud Publica, CISEI, Cuernavaca, Mexico*

TP 050 **Site-directed Nanoprobe-Basecd Affinity Mass Spectrometry for Multiple Biomarkers Identification and Quantitation**; Po-Chiao Lin[3]; Shu-Hua Chen[1]; Avijit Kumar Adak[2]; Mu-Lin Chen[2]; Yu-Ju Chen[1]; Chun-Cheng Lin[2]; *[1]Institute of Chemistry, Academia Sinica, Taipei, Taiwan; [2]Department of Chemistry, Tsing Hua University, Hsinchu, Taiwan; [3]Taiwan International Graduate Program, Taipei, Taiwan*

TUESDAY POSTERS

TP 051 **MALDI-TOF Interrogation of Protein Arrays Facilitated by Patterned Porous Gold Substrates**; Kenyon EVANS-Nguyen; Dwella M Nelson; Sheng-Ce Tao; Heng Zhu; Robert J. Cotter; *Johns Hopkins University, Baltimore, MD*

TP 052 **Functionalized Magnetic Nanoparticle for Rapid Screening and Structure Determination of Small Molecules by MALDI MS**; Mei-Chun Tseng[1]; Rofe-Amor Obena[1]; Ying-Wei Lu[3]; Po-Chiao Lin[4]; Chia-Chun Chen[2]; Chun-Cheng Lin[3]; Yu-Ju Chen[1]; *[1]Institute of Chemistry, Academia Sinica, Taipei, Taiwan; [2]Department of Chemistry, Taiwam Normal University, Taipei, Taiwan; [3]Department of Chemistry, Tsing Hua University, Hsinchu, Taiwan; [4]Taiwan International Graduate Program, Taipei, Taiwan*

TP 053 **Surface-Assisted Laser Desorption/Ionization on Titania Nanotube Arrays**; Chun-Yuan Lo; Wei-Yu Chen; Yu-Chie Chen; *National Chiao Tung University, Hsinchu, Taiwan*

TP 054 **Biochips with Antibodies Immobilized via Traceless Cleavable Linkers for Immunoaffinity Mass Spectrometry by MALDI-TOF-MS**; Mark Stolowitz; *Stratos Biosystems LLC, San Jose, CA*

TP 055 **Sample Preparation and Concentration for MALDI Mass Spectrometry on a Perforated Film or Plate Containing Chromatographic Media**; Mukta M. Shukla[1]; Deepak K. Butani[1]; Ashok K. Shukla[1]; Vladimir M. Doroshenko[2]; Appavu K. Sundaram[2]; *[1]Glygen Corp., Columbia, MD; [2]MassTech, Inc., Columbia, MD*

TP 056 **Combining Tissue Extraction and Off-Line Capillary Electrophoresis-MALDI FTMS for Neuropeptide Analysis using 2,5-Dihydroxybenzoic Acid**; Junhua Wang; Ruibing Chen; Xiaoyue Jiang; Lingjun Li; *University of Wisconsin-Madison, Madison, WI*

TP 057 **MALDI Sample Preparation - The Use of Biomap MS Imaging to Study Electrospray Sample Deposition**; Andy Mahan; Kevin G. Owens; *Drexel University, Philadelphia, PA*

TP 058 **Single-Use Composite MALDI Targets for the Analysis of Synthetic Technical Polymers and Natural Polysaccharides**; Wolfgang Winkler[1]; Werner Balika[2]; Peter Hausberger[2]; Harald Kraushaar[2]; Guenter Allmaier[1]; *[1]Vienna Univ. of Technology, Vienna, Austria; [2]Sony DADC, Anif, Austria*

TP 059 **Negative-Mode MALDI Mass Spectrometry for the Analysis of Pigments using Tetrathiafulvalene as a Matrix**; Daiki Asakawa; Lee Chuin Chen; Kenzo Hiraoka; *University of Yamanashi, Kofu, Japan*

TP 060 **Novel 3-D Sample Plate using Monolithic Capture Media in Collimated-Hole Structures for Interfacing High Capacity Separations with MALDI-TOF**; Stephen J. Hattan; Marvin Vestal; *Virgin Instruments Corporation, Sudbury, MA*

TP 061 **Vacuum MALDI Linear TOF Mass Spectrometry of High Molecular Mass Nanoparticles and Proteins**; Martina Marchetti[1]; Christian Laschober[1]; Ryan Wenzel[2]; Emmanuel Raptakis[3]; Guenter Allmaier[1]; *[1]Vienna University of Technol, Vienna, Austria; [2]CovalX, Zuerich, Switzerland; [3]Shimadzu Biotech, Manchester, UK*

TP 062 **Titania Micropowder and Nanoparticles for In-Vitro Analysis and In-Situ Imaging of Phospholipids by MALDI-MS;** Pawel Lorkiewicz; Marta C. Yappert; *University of Louisville, Louisville, KY*

TP 063 **Comparison of Deposition Methods for MALDI Mass Analysis of Intact Proteins and Tryptic Digests**; Brent Hilker[3]; Kevin Clifford[3]; Drew Sauter[2]; Julie Harmon[3]; John Koomen[1]; *[1]H. Lee Moffitt Cancer Center, Tampa, FL; [2]Nanoliter, Llc, Henderson, NV; [3]University of South Florida, Tampa, FL*

TP 064 **Electrochromatographic Separation of a Model Naturally Occurring Peptide from Multiple Complex Biological Samples for Analysis and Quantification by MALDI-TOF**; Benjamin Katz; *Protein Discovery, Inc., Knoxville, TN*

TP 065 **The Role of Hydrated Water in MALDI with Serine-Doped CHCA**; Mitsuo Takayama; Takashi Nishikaze; *Yokohama City University, Yokohama, Japan*

TP 066 **Comparison of Approaches in Improving MALDI MS Sensitivity**; Lijuan Peng; Zaneer Segu; Joseph Mathai; Gary R. Kinsel; *Southern Illinois University Carbondale, Carbondale, IL*

MALDI / TANDEM MS, 067 - 076

TP 067 **NanoLC-MALDI Orbitrap Coupling Evaluation: An Attempt to Optimized the Acquisition Strategy**; Joelle Vinh; Iman Haddad; Sega Ndiaye; Anne-Marie Hesse; Jean Rossier; *CNRS UMR7637/ESPCI ParisTech, Paris, France*

TP 068 **MALDI–Tandem Mass Spectrometric Analysis of Painted Works of Art**; Michael P. Napolitano[1]; Julie Arslanoglu[2]; Richard A. Yost[1]; *[1]University of Florida, Gainesville, FL; [2]The Metropolitan Museum of Art, New York, NY*

TP 069 **MALDI-Produced Ions Analyzed by Higher Energy Collisional Dissociation (HCD) using an Linear Ion Trap - Orbitrap Mass Analyzer**; Thomas Moehring[1, 2]; Rosa Viner[1, 2]; Viatcheslav V. Kovtoun[1, 2]; Huy Bui[1, 2]; George Stafford[1, 2]; Julian J Phillips[1, 2]; Stevan R. Horning[1, 2]; Kerstin Strupat[1, 2]; *[1]Thermo Fisher Scientific, Bremen, Germany; [2]Thermo Fisher Scientific, San Jose, CA*

TP 070 **Improving the Efficiency of LC-MS-MS Peptide Sequencing using a vMALDI-LTQ Linear Ion Trap Mass Spectrometer**; Mark Wall; Alan A. Doucette; *Dalhousie University, Halifax, Canada*

TP 071 **Analysis of Mitotic Phosphorylation Sites in the Nuclear Pore Complex using a MALDI-LTQ Orbitrap Mass Spectrometer**; Justin Blethrow [2]; Vlad Zabrouskov[2]; Rosa Viner[2]; Joseph Glavy[1]; *[1]Stevens Institute of Tech., Hoboken, NJ; [2]Thermo Fisher Scientific, San Jose, CA*

TP 072 **Rapid Detection and Identification of Pathogenic Neisseria by Atmospheric Pressure MALDI MS-MS**; Seshu Gudlavalleti[1]; Appavu Sundaram[2]; Jane Razumovski[1]; Vladimir M. Doroshenko[2]; *[1]Science and Engineering Serv, Columbia, MD; [2]Masstech, Inc., Columbia, MD*

TP 073 **Modified Silver Nanoparticle as a Hydrophobic Affinity Probe for Analysis of Peptides and Proteins by using MALDI Mass Spectrometry**; Hui-Fen Wu; Kamlesh Shrivas; *Chemistry department, National Sun Yat-Sen Univers, Kaohsiung, Taiwan*

TP 074 **Direct Analyses of UV Absorbents in Polymer Film by MALDI-TOF MS-MS in Comparison with ESI and APPI MS-MS Analyses**; Shouxun Zhao; Bogdan Piatek; Huayi Tong; *Ciba Corp, Tarrytown, NY*

TP 075 **Formation of Gas Phase Silver Anions and Silver–Iodide Radical Anions by Laser Ablation**; Timothy Dunne; Athula B. Attygalle; *Stevens Institute of Technology, Hoboken, NJ*

TP 076 **A Comparison of LC-MALDI and LC-ESI for the Analysis of a Highly Complex Mixture of Peptides**; Keith Ashman; Mitchell Isaacs; Xiaomin Song; Chris Clark; Lewis Adler; *APAF, Sydney, Australia*

ECD/ETD/EDD, 077 - 090

TP 077 **Data-Dependent Supplemental Activation to Enhance ETD Efficiency for High M/Z Precursors Regardless of Charge**; Aaron Ledvina; Graeme McAlister; Joshua J. Coon; *The University of Wisconsin, Madison, WI*

TP 078 **High-Energy Electron Transfer Dissociation (ETD) on Collision with Alkali Metal Targets**; Shigeo Hayakawa [1]; Mami Hashimoto[1]; Hirofumi Nagao[2]; Michisato Toyoda[2]; *[1]Osaka Prefecture Univ., Sakai, Osaka, Japan; [2]Osaka University, Toyonaka, Japan*

TP 079 **Effect of Ion Activation on Radical Driven Reactions in Electron Capture Dissociation**; Cheng Lin; Jason J Cournoyer; Xiaojuan Li; Peter B. O'connor; *Boston University School of Medicine, Boston, MA*

TP 080 **Electron Detachment Dissociation in a Hybrid Radio Frequency Linear Ion Trap/Time of Flight Mass Spectrometer**; Travis F. Greene[1]; Jared M. Bushey[1]; Takashi Baba[2]; Gary L. Glish[1]; *[1]University of North Carolina, Chapel Hill, NC; [2]University of North Carolina and Hitachi, Ltd., Tokyo, Japan*

TP 081 **Modeling of Metastable Atoms and Protonated Peptide Ions Interaction**; Vadym Berkout[2]; Sergey Kryuchkov[1]; Vladimir M. Doroshenko[2]; *[1]University of Calgary, Calgary, Canada; [2]MassTech, Inc., Columbia, MD*

TP 082 **Electron Transfer Dissociation Facilitates the Measurement of Deuterium-Incorporation into Selectively Labeled Peptides with Single Residue Resolution**; Martin Zehl; Kasper D. Rand; Ole N. Jensen; Thomas J. D. Jørgensen; *University of Southern Denmark, Odense, Denmark*

TP 083 **ECD within a Linear Magnetic (no-RF) Cell**; Valery G. Voinov; Max L. Deinzer; Douglas F. Barofsky; *Oregon State University, Corvallis, OR*

TP 084 **Multistage Electron Capture Dissociation for the Investigation of Charge Reduced Peptide Ions**; Takashi Baba[1]; Jared Bushey[2]; Gary L. Glish[2]; *[1]University of North Carolina and Hitachi, Ltd.,, Tokyo, Japan; [2]University of North Carolina, Chapel Hill, NC*

TP 085 **Electron Capture/Transfer Dissociation of Alpha-Helical Peptides: Characteristic Features and Interpretation**; Yury O. Tsybin [1]; Hisham Ben Hamidane[1]; Aleksey Vorobyev[1]; Adrien Schmid[1]; Oleg Yu. Tsybin[2]; Clemence Corminbeuf[1]; Vincent Pouthier[3]; *[1]EPFL (Ecole Polytechnique Federale de Lausanne), Lausanne, Switzerland; [2]State Polytechnical University, Saint-Petersburg, Russian Federation; [3]Universite de Franche-Comte, Besancon, France*

TP 086 **Hot Electron Capture Dissociation in a Linear Radio Frequency Quadrupole Ion Trap**; Naomi Manri [1]; Hiroyuki Satake[1]; Takashi Baba[1]; Kuriko Yamada[2]; Hiroaki Nakagawa[2]; Kisaburo Deguchi[2]; *[1]Hitachi, Ltd., Kokubunji, Japan; [2]Univ, Hokkaido, Sapporo, Japan*

TP 087 **ECD, EDD and CID of Polyamidoamine (PAMAM) Dendrimer Ions with Amino, Amidoethanol and Sodium Carboxylate Surface Groups;** Malgorzata A Kaczorowska; Helen Cooper; *University of Birmingham, Birmingham, UK*

TP 088 **Electron Current and Kinetic Energy Effects on the Electron Detachment Dissociation of Glycosaminolgycan Carbohydrates**; Franklin E. Leach III[1]; Jeremy Wolff[1]; Tatiana Laremore[2]; Robert J. Linhardt[2]; Jon Amster[1]; *[1]University of Georgia, Athens, GA; [2]Rensselaer Polytechnic Institute, Guilderland, NY*

TP 089 **Evaluation of Electron Transfer Dissociation in a Hybrid Quadrupole-Hexapole Fourier Transform Ion Cyclotron Resonance Mass Spectrometer**; Desmond A. Kaplan[1]; Ralf Hartmer[2]; Michael L. Easterling[1]; Jiong Yang[1]; Melvin A. Park[1]; *[1]Bruker Daltonics, Inc., Billerica, MA; [2]Bruker Daltronik, Bremen, Germany*

TP 090 **Electron Transfer Dissociation of iTRAQ Labeled Peptide Ions**; Hongling Han [1]; Darryl J. Pappin[2]; Scott A. McLuckey[1]; *[1]Purdue University, West Lafayette, IN; [2]Applied Biosystems, Foster City, CA*

EMERGING CONTAMINANTS 1, 091 - 109

TP 091 **Characterization of Dissolved Protein in Seawater using LTQ-FT MS**; Yuchen Lu; Brent, Reschke; Kathleen Kelly; Aaron Timperman; *West Virginia University, Morgantown, WV*

TP 092 **MALDI-ToF MS Used for Fast Detection of *Legionella* Species in Water Supplies: A New Rapid Response to Legionellosis**; Xaviera Pennanec; *Laboratoire CGI, Ploemeur, France*

TP 093 **Quantitation of Perchlorate, Nitrate, Thiocyanate and Iodide in Infant Urine from Disposable Diapers**; Samaret Otero; Liza Valentin-Blasini; Benjamin Blount; *Centers for Disease Control and Prevention, Atlanta, GA*

TP 094 **Integrated Disinfection By-Products Mixtures Research: Results from the Four Lab Study**; Jane Ellen Simmons[1]; Susan Richardson[2]; Michael G. Narotsky[1]; Larry D. Claxton[1]; E. Sidney Hunter III[1]; Richard J. Miltner[1]; Jonathan Pressman[1]; Thomas F. Speth[1]; Glenn Rice[1]; Linda K. Teuschler[1]; Stuart W. Krasner[4]; Howard S. Weinberg[3]; *[1]U.S. EPA, RTP, NC, NC; [2]Us Epa, Athens, GA; [3]University of North Carolina, Chapel Hill, NC; [4]Metropolitan Water District of Southern California, LaVerne, CA*

TP 095 **Multidimensional Analysis of Environmental Samples: Gas Chromatography/Fourier Transform Ion Cyclotron Resonance Mass Spectrometry and Ab-Initio Calculations**; Indira Silwal; Jayendran C. Rasaiah; Touradj Solouki; *University of Maine, Orono, ME*

TP 096 **Evidences of the Existence of Multiple Charged Constituents in Suwannee River Dissolved Organic Matter**; Andras Gaspar[15]; Erast Kunenkov[3]; Richard Lock[2]; Michael Desor[4]; Irina Perminova[3]; Philippe Schmitt-kopplin[15]; *[1]Helmholtz Zentrum münchen, Neuherberg, Germany; [2]Waters Corporation, Manchester, England; [3]Lomonosov Moscow State University, Moskow, Russia; [4]Waters, Eschborn, Germany; [5]Helmholtz Zentrum München, Neuherberg, Germany*

TP 097 **Characterization of Natural Organic Matter in Raw Water with QTOF Mass Spectrometry**; Douglas B. Mawhinney; Fernando L. Rosario-Ortiz; Seungyun Baik; Brett J. Vanderford; Shane A. Snyder; *Southern Nevada Water Authority, Las Vegas, NV*

TP 098 **Illicit Drugs and their Metabolites as Environmental Contaminants**; Roberto Fanelli; Sara Castiglioni; Chiara Chiabrando; Renzo Bagnati; Ettore Zuccato; *Mario Negri Institute, Milano, Italy*

TP 099 **The Silica Speciation by FAB-MS for the Uptake to the Diatom: Photic Layer of Tokyo Bay**; Miho Tanaka[1]; Kazuya Takahashi[2]; Masao Nemoto[1]; Hideki Nagashima[1]; *[1]Tokyo University of Marine Science and*

Technology, Minato-ku, Tokyo, Japan; [2]Riken, Wako-shi, Saitama, Japan

TP 100 **Characterization of Organic Matter in a Waste Landfill Leachate**; Laurent Badoil[1]; David Benanou[1]; Jean-claude Tabet[2]; Denis Lesage[2]; *[1]Anjou Recherche, Maisons-Laffitte, France; [2]University Paris Vi (upmc), Paris, France*

TP 101 **Detection of Cyanobacterial Peptide Toxins Microcystins in Exposed Animal Tissues by the MMPB Method and LC-MS-MS**; Milla-Riina Neffling[1]; Emilie Lance[2]; Jussi AO Meriluoto[1]; *[1]Åbo Akademi University, Turku, Finland; [2]University of Rennes, Rennes, France*

TP 102 **Quantitative Analysis of Perchlorate by Ion Chromatography MS-MS**; Mathew Johnson[3]; Jay Gandhi[2]; Sheher Mohsin[1]; *[1]Agilent Technologies, Schaumburg, IL; [2]Metrohm-peak Llc, Houston, TX; [3]USEPA Region 6, Houston, TX*

TP 103 **Determination of Haloacetic Acids in Drinking Water using Liquid Chromatography / Tandem Mass Spectrometry**; Shueh-Ni Chang; Chia-Yang Chen; *National Taiwan University, Taipei City, Taiwan*

TP 104 **Determination of Macrocyclic Trichothecenes in a Water Damaged House by LC-MS**; Masahiko Takino[1]; Yoshiko Sugita-Konishi[2]; James J Pestka[3]; *[1]Agilent Technologies, Hachioji-shi, JAPAN; [2]National Institute of Health Sciences, Tokyo, Japan; [3]Michigan State University, East Lansing, MI*

TP 105 **Characterization of Dissolved Organic Matter in Marine Pore Waters by Fourier Transform Ion Cyclotron Resonance Mass Spectrometry**; Frauke Schmidt[3]; Boris Koch[2]; Marcus Elvert[3]; Matthias Witt[1]; Kurt Haag [4]; Kai-Uwe Hinrichs[3]; *[1]Bruker Daltonik GmbH, Bremen, Germany; [2]Alfred-Wegener Institute, Bremerhaven, Germany; [3]Bremen University, Bremen, Germany; [4]Bruker Daltonics, Shoreline, WA*

TP 106 **HPLC-MS-MS Determination of Nine N-Nitrosamines in Thirty-Nine North American Drinking Water Systems**; Jessica M. Boyd[1]; Yuan-yuan Zhao[1]; Feng Qin[1]; Patrick Levallois[3]; Susan Richardson[2]; Xing-fang Li[1]; *[1]University of Alberta, Edmonton, Canada; [2]US EPA, Athens, GA; [3]Institut National de Sante Publique du Quebec, Quebec, Canada*

TP 107 **Determination of Perchlorate in River by Electrospray Ionization Tandem Mass Spectrometry Following Ion-Pair Hollow-Fiber Liquid-Phase Microextraction**; Wen-Tsen Chen; Hsin-Chang Chen; Wang-Hsien Ding; *National Central University, Chung-li, Taiwan*

TP 108 **The Influence of Substrate Levels, Temperature, pH, Inorganic Salts on the Yield of Disinfection By-Products in Aquatic Chlorination of Anisole**; Olga Polyakova; Alina Bobrel; Albert T. Lebedev; *Moscow State University, Moscow, Russian Federation*

TP 109 **Simultaneous Analysis of Iodoacetic Acids, Bromoacetic Acids and Other Halogenated Compounds in Water using Ion Chromatography/Inductively Coupled Plasma/Mass Spectrometry (IC/ICP/MS)**; Honglan Shi[1]; Craig D. Adams[2]; *[1]Missouri S&T/ERC, Rolla, MO; [2]Missouri University of Science and Technology, Rolla, MO*

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TP 111 **Laser Desorption 7.87 eV Postionization Mass Spectrometry of Cysteine-Containing Peptides by Pyrenyl Tagging**; Luke Hanley[2]; Artem Akhmetov[2]; Gerald Gasper[2]; Jerry F. Moore[1]; *[1]Massthink LLC, Naperville, IL; [2]University of Illinois at Chicago, Chicago, IL*

TP 112 **Concise Representation of MS Images by Probabilistic Latent Semantic Analysis**; Michael Hanselmann[1]; Bernhard Y. Renard[1]; Marc Kirchner[1]; Andriy Kharchenko[2]; Lennaert Klerk[2]; Ullrich Koethe[1]; Ron M.a. Heeren[2]; Fred Hamprecht[1]; *[1]University of Heidelberg, Heidelberg, Germany; [2]Fom Inst. Atomic/molecular Physics, Amsterdam, Netherlands*

TP 113 **Enhanced Interpretation of Imaging Mass Spectrometry Data using Non-negative Matrix Factorization**; Raf Van de Plas; Bart Vanluyten; Bart De Moor; Etienne Waelkens; *K.U.Leuven, Leuven, Belgium*

TP 114 **Improvement on Sensitivity of High-Spatial-Resolution Mass Imaging Based on MALDI-QIT-TOF-Type Mass Spectrometer**; Osamu Furuhashi; Hideaki Izumi; Takahiro Harada; Kengo Takeshita; Kiyoshi Ogawa; Yoshikazu Yoshida; *Shimadzu Corporation, Soraku-gun, Japan*

TP 115 **Laser Desorption 7.87 eV Postionization Mass Spectrometry of Antibiotics in *S. epidermidis* Bacterial Biofilms**; Gerald Gasper[3]; Ross Carlson[2]; Artem Akhmetov[3]; Jerry F. Moore[1]; Luke Hanley[3]; *[1]MassThink LLC, Naperville, IL; [2]Montana State University, Bozeman, MT; [3]University of Illinois at Chicago, Chicago, IL*

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TP 117 **Hierarchical Clustering: A New Approach using Unsupervised Classification of MALDI Imaging Data for Cancer Biomarker Detection in Tissue**; Axel Walch[3]; Sören-Oliver Deininger[1]; Shi Gongyi[2]; Michael Becker[1]; Martin Schürenberg[1]; Arne Fütterer[1]; Marc Gerhard[1]; Detlev Suckau[1]; *[1]Bruker Daltonik GmbH, Bremen, Germany; [2]Bruker Daltonics, Freemont, CA; [3]GSF-Institut für Pathologie, Munich, Germany*

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TP 119 **Enhancements in Analysis and Imaging of Small Molecules in Tissue by MALDI-MS Afforded by Prolonged Sample Storage at Reduced Pressure**; Hazel R Dickson; Josephine Bunch; Cameron W. Mcleod; *University of Sheffield, Sheffield, UK*

TP 120 **Automatic Spotting Solution for MALDI Imaging: Process Optimization and New Developments**; Julien Franck[1]; Maxence Wisztorski[1]; Mohamed El-Ayed[1]; David Bonnel[1]; Alan Barnes[2]; Isabelle Fournier[1]; Michel Salzet[1]; *[1]University of Lille 1, Fre-cnrs 2933, Ifr 147, Villeneuve D'ascq Cedex, France; [2]Shimadzu Biotech, Manchester, UK*

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TP 125 **Adapting the Stretch Sample Method from Tissue Profiling to Imaging**; Tyler A Zimmerman; Eric Monroe; Jonathan Sweedler; *University of Illinois at Urbana-Champaign, Urbana, IL*

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TP 130 **What's New with the 5 Pump, 4 Detector LC-MS Based Purification Systems at Lundbeck**; Xu Zhang; David P Budac; Mark J. Hayward; *Lundbeck Research USA, Stockton, NJ*

TP 131 **Solid Phase Extraction - Liquid Chromatography (SPE-LC) Interface for Automated Peptide Separation and Identification by Tandem Mass Spectrometry**; O.B. Hoerning; M.B. Andersen; O. Vorm; *Proxeon A/S, Odense, Denmark*

TP 132 **Fingerprint Analysis of Intact Cells using a Microfluidic Chip Coupled with MALDI-TOF MS**; Jeonghoon Lee; Steven A. Soper; Kermit K. Murray; *Louisiana State University, Baton Rouge, LA*

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TP 134 **Walk Up UPLC-MS for Rapid High Quality Sample Analysis in Support of Discovery Chemistry**; Bethanne Warrack[1]; Dieter Drexler[3]; Chiuwa Emily Luk[2]; *[1]Bristol-Myers Squibb, Princeton, NJ; [2]Bristol-Myers Squibb Co, Princeton, NJ; [3]Bristol Myers Squibb, Wallingford, CT*

TP 135 **An Integrated Approach for an Ultra-High Throughput On-Line SPE-MS-MS System and its Applications to ADME Assays**; Rongda Xu; Marianne T. Quintos; Melinda Manuel; Joshua E. Cramlett; Kheng B. Lim; Daniel B. Kassel; *Takeda San Diego, Inc., San Diego, CA*

TP 136 **Understanding the Use of Temperature Regulation to Optimize Mass Transfer in Fast Gradient Reversed Phase Liquid Chromatography**; Mark J. Hayward; *Lundbeck Research USA, Stockton, NJ*

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TP 139 **Automated Purification and Sample Preparation Robot for Lab and Portable Mass Spec Analysis**; David P Fries; Brian P Gregson; Stan Ivanov; Matthew Smith; James Wilson; *U South Florida, St Petersburg, FL*

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TP 155 **Multiplex Enzyme Inhibition Screening via MALDI-3Q-MS;** Kenneth D. Greis[1]; Rakesh Rathore[1]; George Scott[2]; Pauline J. Vollmerhaus[2]; Jay Corr[2]; *[1]University of Cincinnati, Genome Research Inst., Cincinnati, OH; [2]MDS Sciex, Concord, ON*

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TP 170 **Isolation and Chemical Characterization of the Extracellular Polysaccharide Required for Biofilm Formation in Bacillus Subtilis**; Ahmed Hussein[1]; Daniel Kearns[2]; Yehia Mechref[1]; Milos Novotny[1]; *[1]National Center for Glycomics and Glycoproteomics, Bloomington, IN; [2]Biology Department Indiana University, Bloomington, IN*

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TP 173 **The False Positive Rates Associated with the Methods Currently Used to Identify Sites of N-linked Glycosylation**; Lei Cheng[1]; Art Nuccio[1]; James A Atwood III[2]; D. Brent Weatherly[2]; Ron Orlando[1]; *[1]University of Georgia, Athens, GA; [2]BioInquire, Athens, GA*

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TP 192 **Analysis of Intracellular Lipid Hydroperoxide-Mediated Oxidative Stress by Stable Isotope Dilution LC-MS**; Ian A. Blair[1]; Peijuan Zhu[2]; *[1]Univ. of Penn/Center for Can, Philadelphia, PA; [2]Schering Plough, Clark, NJ*

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TP 195 **Profiling of Yeast Sphingolipids by LC-MS-MS to Study the Regulation of Ceramide Synthesis in Cells Impaired for TORC2 Activity;** Sofya Aronova; Karen Wedaman; Pavel Aronov; Karmela Ramos; Bruce D Hammock; Ted Powers; *UC Davis, Davis, CA*

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TP 198 **Quantification of Phosphatidylcholine Molecular Species in Bile by Electrospray Ionization Tandem Mass Spectrometry**; Wujuan Zhang[1]; Hector Vilca-Melendez[2]; Kenneth Setchell[1]; *[1]Cincinnati Children's Hospital Medical Center, Cincinnati, OH; [2]King's College Hospital, London, UK*

TP 199 **Following the Oxidation and Thermal Decomposition of Edible Oils using MALDI-TOF Mass Spectrometry**; Jennifer Gidden; Rohana Liyanage; Jack Lay; *Univeristy of Arkansas, Fayetteville, AR*

TP 200 **Targeted and Global Glycerophospholipid Nano ESI-MS Analysis of Liver Tissue Extracts in Patients with Non-alcoholic Steatohepatitis**; Jane Zhao[1]; Bianca M. Arendt[2]; David W. L. Ma[3]; Brigitte Simons[1]; Duchoslav Eva[1]; Elaheh Aghdassi[2]; Johane Allard[2]; *[1]Applied Biosystems/MDS Sciex, Concord, Ontario; [2]Gastroenterology and Nutrition, Univ of Toronto, Toronto, Ontario; [3]University of Guelph, College of Biological Sci, Guelph, Ontario*

TP 201 **Direct Analysis of Lipids and Other Metabolites in Mouse Brain Tissue with Infrared Laser Ablation and Mass Spectrometry**; Bindesh Shrestha[1]; Peter Nemes[1]; Javad Nazarian[2]; Eric P. Hoffman[2]; Akos Vertes[1]; *[1]George Washington University, Washington, DC; [2]Children's National Medical Center, Washington, DC*

TP 202 **Determination of Pyrophosphorylated Forms of Lipid A in Gram-Negative Bacteria using a Multi-Faceted Mass Spectrometric Approach**; Jace W. Jones[1]; Andrew G. Baker[2]; Scott A. Shaffer[1]; Robert K. Ernst[1]; David R. Goodlett[1]; Frantisek Turecek[1]; *[1]University of Washington, Seattle, WA; [2]Waters, Inc., Dublin, CA*

TP 203 **Negative Ion Pencil Lead Maldi and MALDI MS-MS for the Identification and Structural Analysis of Free Fatty Acids**; Douglas J.H Olson; Mark A Smith; Melanie Dauk; Darwin W Reed; Suzanne R Abrams; *National Research Council, Saskatoon, Canada*

TP 204 **HPLC-MS Analysis of Various Phospholipid Classes**; Miroslav Lísa; Eva Cánová; Michal Holcapek; *University of Pardubice, Pardubice, Czech Republic*

TP 205 **Triacylglycerolomics - Characterization of Complex Triacylglycerol Mixtures in Plant Oils and Animal Fats**; Michal Holcapek; Miroslav Lisa; *University of Pardubice, Pardubice, Czech Republic*

TP 206 **On-line Normal-Phase Chromatography LC-MS with a FTICR MS: Accurate Mass Measurement Approach for Lipid Analysis**; Yewon Lee; Han-Bin Oh; *Sogang University, Seoul, Korea*

TP 207 **An Automated Workflow for Rapid Alignment and Identification of Lipid Biomarkers Obtained from Chip-Based Direct Infusion Nanoelectrospray Tandem Mass Spectrometry**; Jens Hoefkens [1]; Tobias Kind[2]; Kent Pinkerton[3]; Oliver Fiehn[2]; *[1]Genedata Inc, Waltham, MA; [2]UC Davis - Metabolomics, Davis, CA; [3]UC Davis Center for Health and the Environment, Davis, CA*

TP 208 **Lipid Analysis of Archaeological Nabatean Lamps using nanoESI-Qq-FT-ICR MS**; Caroline Tokarski[1]; Nicolas Garnier[2]; Christian Rolando[1]; *[1]Univ. des Science/Tech de Lille, Villeneuve d'Ascq, France; [2]Laboratoire Nicolas Garnier, Vic-le-Comte, France*

TP 209 **Metabolic Profiling of Phospholipids in Rat Plasma utilizing Ultra Pressure Liquid Chromatography and oa TOF Mass Spectrometry**; Rob Plumb [1]; Paul Rainville[1]; John P Shockor[2]; Chris L. Stumpf[2]; *[1]Waters, Milford, MA; [2]Waters Corporation, Milford, MA*

TP 210 **Dissociation of Copper(I) and Silver(I) Cluster Ions of Fatty Acids: Ag_2H^+ as a Marker for Double Bonds;** Voislav Blagojevic; Laura Banu; Diethard K. Bohme; *York University, Toronto, Canada*

TP 211 **Identification and Quantification of Abundant Alkyl Ether Phospholipids in the Human Lens: A Shotgun Lipidomics Approach using Ozone Induced Dissociation**; Jane M. Deeley[1]; Todd W Mitchell[1]; Michael Thomas[1]; Roger J.W. Truscott[2]; Stephen J Blanksby[1]; *[1]University of Wollongong, Wollongong, Australia; [2]Save Sight Institute, University of Sydney, Sydney, Australia*

TP 212 **ESI-MS of Retinal Phosphatidylcholines in a Stargardt Disease-3 Mouse Model;** Shelley N. Jackson[1]; Anne McMahon[2]; Amina S. Woods[1]; Wojciech Kedzierski[2]; *[1]NIDA-IRP, NIH, Baltimore, MD; [2]The University of Texas Southwestern Medical Center, Dallas, TX*

TP 213 **The Influence of different Detergents on Spermatozoa Membrane Solubilization and the subsequent Phospholipid Analysis by MALDI-TOF Mass Spectrometry**; Beate Fuchs[1]; Ulrike Jakop[2]; Karin Müller[2]; Rosemarie Süß[1]; Jürgen Schiller[1]; *[1]University of Leipzig, Leipzig, Germany; [2]Leibniz Institute for Zoo and Wildlife Research, Berlin, Germany*

TP 214 **CID/OzID: A New Ion Activation Approach for the Assignment of sn-Position in Phospholipids**; Michael Thomas; Todd W Mitchell; Stephen J Blanksby; *University of Wollongong, Wollongong, NSW, Australia*

TP 215 **Identification of Significant Acylation Pattern Changes in Lipid A species from Escherichia coli lpxL- Mutants Grown at High Temperatures;** Birgit Schilling[1]; Michael A Apicella[2]; Bradford W. Gibson[1]; *[1]Buck Institute for Age Research, Novato, CA; [2]University of Iowa, Iowa City, IA*

TP 216 **Analysis of N-Acylphosphatidylethanolamine using Electrospray Ionization Tandem Mass Spectrometry**; Giorgis Isaac [1]; Aruna Kilaru[2]; Peter Koulen[3]; Kent Chapman[2]; Ruth Welti[1]; *[1]Kansas State University, Manhattan, KS; [2]University of North Texas, Denton, TX; [3]University of North Texas Health Science Center, Fort Worth, TX*

TP 217 **Characterization of Yeast Glycerophospholipid Composition by HPLC/ESI-FTICR-MS**; Heiko Hayen; Eva-M. Hein; *ISAS - Institute for Analytical Sciences, Dortmund, Germany*

TP 218 **Modulation of Gangliosides in U373MG Glioblastoma by ST6GalNacV Gene Transfection**; Mark R. Emmett[1]; Huan He[2]; Carol L. Nilsson[3]; Alan G. Marshall[5]; Roger A. Kroes[4]; Mary Schmidt[4]; Joseph R. Moskal[4]; *[1]Nat'l High Magnetic Field Lab, Tallahassee, FL; [2]Florida State University, Tallahassee, FL; [3]Pfizer, Inc., San Diego, CA; [4]The Falk Center for Molecular Therapeutics, Evanston, Illinois; [5]Ion Cyclotron Resonance Prog, Tallahassee, FL*

TP 219 **Qualitative and Quantitative Analysis of Lipid Classes from 2 Different Sources using Electrospray Ionization and High Resolution LC-MSn Mass Spectrometry**; Laurance Lee; Donna L. Wilson; Anne Ferguson; *Thermo Fisher Scientific, Inc., San Jose, CA*

TP 220 **Identifying Lipids and Other Small Molecules from Imaging Mass Spectrometry Experiments using Tandem Mass Spectrometry and Exact Mass**; Timothy Garrett [1]; Ming Gu[2]; William W. Dawson[1]; David H. Powell[1]; Richard A. Yost[1]; *[1]University of Florida, Gainesville, FL; [2]Cerno Bioscience, Yardley, PA*

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TP 222 **Clustering Software for Analysis of Complex Lipid Profile Data Based on Detection of Fish Oils by MALDI Mass Spectrometry**; Helen Montgomery[1]; Gerald Stubiger[2]; Wolfgang Werther[3]; Emmanuel Raptakis[4]; Omar Belgacem[4]; *[1]Shimadzu, Koichi Tanaka MS Research laboratory, Manchester, UK; [2]Medical University of Vienna, Vienna, Austria; [3]University of Vienna, Vienna, Austria; [4]Shimadzu Biotech, Manchester, UK*

TP 223 **Lipidomic Analysis and Comparison of Mitochondrial and Plasma Membrane Fatty Acid Profiles Isolated From Various Tissues**; Michael D. Timmons; Shuling Xiong; Mark A. Lovell; Bert C. Lynn; *University of Kentucky, Lexington, KY*

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TP 225 **Protein-Oligonucleotide Complexes Characterization using Noncovalent Mass Spectrometry: Study of the tRNA Binding Properties of tRNA m1A58 Methyltransferase;** Cédric Atmanene[1]; Pierre Barraud[2]; Frédéric Dardel[2]; Carine Tisne[2]; Alain Van Dorsselaer[1]; Sarah Sanglier[1]; *[1]IPHC-DSA, ULP, CNRS, Strasbourg, France; [2]Laboratoire de Cristallographie et RMN biologiques, Paris, France*

TP 226 **Comparative Thermodynamic Study of the Human ABO(H) Blood Group Glycosyltransferases using nanoES-FTICR-MS**; Naoto Soya[1]; Glen Shoemaker[1]; Monica Palcic[2]; John S Klassen[1]; *[1]University of Alberta, Edmonton, Canada; [2]Carlsberg Laboratory, Copenhagen, Denmark*

TP 227 **Determining a Molecular Pathway for Formation of a T=3 Capsid using ESI-MS and ESI-IMS-MS**; Victoria L Morton; Peter G Stockley; Nicola Stonehouse; Alison E. Ashcroft; *University of Leeds, Leeds, UK*

TP 228 **DNA-Nuclear Receptor Interaction Studied by Mass Spectrometry**; Claudia Bich[1]; Cédric Bovet[1]; Natacha Rochel[2]; Carole Peluso-Iltis[2]; Ryan Wenzel[1]; Dino Moras[2]; Renato Zenobi[1]; *[1]ETH Zurich, Zurich, Switzerland; [2]Inst. Génétique et Biologie Mol. et Cell., Illkirch, France*

TP 229 **Quantitative Determination of Metal-Protein Dissociation Constants using Metal-Catalyzed Oxidation Reactions and Mass Spectrometry**; Adam M Graichen; Richard Vachet; *University of Massachusetts, Amherst, MA*

TP 230 **A Comparison of Specific and Nonspecific Protein-Ligand Interactions using FTICR MS**; Michelle Sweeney; John R. Eyler; *University of Florida, Gainesville, FL*

TP 231 **Ion Mobility Mass Spectrometry and Proton Transfer Reactions of Non-covalent Amyloid β-protein Oligomers**; Eric S. Pang; Rachel O. Loo; Sheng Yin; Pinmanee Boontheung; David B. Teplow; Joseph A. Loo; *UCLA, Los Angeles, CA*

TP 232 **SUPREX Analysis of a Misfolded Disease-Related Variant of Alanine:Glyoxylate Aminotransferase**; Erin D. Hopper; Adrianne M.C. Pittman; Chandra Tucker; Michael C. Fitzgerald; *Duke University, Durham, NC*

TP 233 **High-Mass MALDI MS: Characterization of Large Molecular Size Hemoglobin-Based Oxygen Carriers**; Tatiana Pimenova[1]; Claudia Pereira[2]; Dominik Schaer[2]; Renato Zenobi[1]; *[1]ETH Zurich, Zurich, Switzerland; [2]Medical Clinic Research Unit, University of Zurich, Zurich, Switzerland*

TP 234 **The Analysis of the Interactions and Complexation of Polycyclic Aromatic Hydrocarbons and Cyclodextrin using Electrospray Ionization Mass Spectrometry**; Andrew Harron[1]; Catherine Bentzley[1]; Preston Moore[1]; Darryl Davis[2]; *[1]University of the Sciences in Philadelphia, Philadelphia, PA; [2]Centocor, Collegeville, PA*

TP 235 **Development of an ESI-MS Method for DNA-Ligand Screening Applied to Recognition of T:G Mismatched Base Pairs**; Federico Riccardi Sirtori[1]; Roberto D'Alessio[1]; Giancarlo Aldini[2]; Maristella Colombo[1]; *[1]Nerviano Medical Sciences, Nerviano, Italy; [2]Faculty of Pharmacy, University of Milan, Milan, Italy*

TP 236 **NanoESI-Mass Spectrometry: A Versatile Tool for a Fast Affinity Classification of Clinical Inhibitors of Human Kinases**; Matthias Jecklin[1]; David Touboul[1]; Rishi Jain[2]; Estee Naggar[2]; John Tallarico[2]; Paul Ramage[3]; Peter Drueckes[3]; Renato Zenobi[1]; *[1]ETH Zurich, Zurich, Switzerland; [2]Novartis Institutes for BioMedical Research, Cambridge, MA; [3]Novartis Institutes for BioMedical Research, Basel, Basel, Switzerland*

TP 237 **Mass Spectrometry and Ion Mobility of Noncovalent Alpha-Synuclein-Ligand Complexes: Determination of Ligand Binding Sites and Protein Conformations**; Sheng Yin; Joseph A. Loo; *UCLA, Los Angeles, CA*

TP 238 **Native and Denaturation Products of 9 MegaDalton Vault Complexes Characterized by Ion Mobility Mass Spectrometry**; Shirley H. Lomeli; Catherine S. Kaddis; Sheng Yin; Rachel R. Ogorzalek Loo; Leonard H. Rome; Joseph A. Loo; *University of California, Los Angeles, Los Angeles, CA*

TP 239 **Anion Recognition of Glycocalix[4]arenes Studied by ESI-FTICR Mass Spectrometry**; Mika J. Torvinen [1]; Elina Kalenius[1]; Francesco Sansone[2]; Alessandro Casnati[2]; Rocco Ungaro[2]; Pirjo Vainiotalo[1]; *[1]University of Joensuu, Joensuu, Finland; [2]Università di Parma, Parma, Italy*

TP 240 **Quantifying Protein-Hydrophobic Ligand Interactions by ES-MS**; Lan Liu; John S. Klassen; *University of Alberta, Edmonton, Canada*

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Nichiporuk; Anna M. Zawadzka; Ulla Norklit Andersen; Kenneth N. Raymond; *University of California, Berkeley, Berkeley, CA*

TP 242 **Stereochemical Effects of Substituents in Position 11 of 17-Beta-Estradiol on Gas Phase Acidity: A Cooperative Effect**; Sandrine Voillard[1]; Françoise Fournier[1]; Yves Jacquot[1]; Carlos Afonso[1]; Guy Leclercq[2]; Jean-Claude Tabet[1]; *[1]University Paris VI (UPMC), Paris, France; [2]Institut Jules Bordet, Brussels, Belgium*

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TP 244 **Characterization of a Novel Cross-linkage in Actinomyces naeslundii Fimbriae using C-terminal Ladder Sequencing Approaches and Mass Spectrometry**; Jenny T.C. Ho[1]; Sonja Hess[1]; John O Cisar[2]; *[1]Caltech, Pasadena, CA; [2]NIDCR, National Institutes of Health, Bethesda, MD*

TP 245 **Characterization of *Enterococcus faecium* peptidoglycan: Understanding Biosynthesis and Antibiotic Binding Sites**; Jiawei Chen; Gary Patti; Jacob Schaefer; Michael L. Gross; *Washington University in St. Louis, St. Louis, MO*

TP 246 **Immobilization of Microorganisms with Cationic Nanoparticles for Detection by Mass Spectrometry**; Cheng-Tung Chen[1]; Anren Hu[2]; Chia-Liang Cheng[1]; Yen-peng Ho[1]; *[1]National Dong Hwa University, Hualien, Taiwan; [2]Tzu Chi University, Hualien, Taiwan*

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TP 249 **Detection and Discrimination of Extended-Spectrum β-lactamase (ESBL) Producing Bacteria by MALDI-TOF-MS**; Ian Edwards[4]; Edina Chiriseri[2]; Marilena Ioannou[1]; Ruta Furmonaviciene[1]; Colin Geary[3]; Richard O Jenkins[1]; *[1]De Montfort University, Leicester, UK; [2]Northampton General Hospital, Leicester, UK; [3]Leicester Royal Infirmary, Leicester, UK; [4]Shimadzu Biotech / Kratos Analytical Ltd, Manchester, UK*

TP 250 **Discrimination of *Aspergillus* Isolates at the Species and Strain Level by MALDI-TOF Mass Spectrometry Fingerprinting**; Amanda D. Buskirk; Justin M. Hettick; Brett J. Green; Michael L. Kashon; James E. Slaven; Erika Janotka; Detlef Schmechel; Donald H. Beezhold; *NIOSH, Morgantown, WV*

TP 251 **MALDI Mass Spectrometry Detection of Plant Pathogenic Bacteria**; Anja Freiwald; Magdalena Kliem; Sascha Sauer; *MPI for Molecular Genetics, Berlin, Germany*

TP 252 **Catching the Evolution of a Killer Virus with Mass Spectrometry**; Bethny Morrissey; Alexander Schwahn; Margaret Streamer; Kevin Downard; *University of Sydney, Sydney, Australia*

TP 253 **Discrimination of *Penicillium* isolates by MALDI-TOF Mass Spectrometry Fingerprinting**; Justin M. Hettick; Amanda D. Buskirk; Brett J. Green; Michael L. Kashon; James E. Slaven; Erika Janotka; Detlef Schmechel; Donald H. Beezhold; *NIOSH, Morgantown, WV*

TP 254 **Rapid Method for Sensitive Screening of Oligosaccharide Epitopes in the *Campylobacter jejuni* Strains Isolated from Guillain-Barré Syndrome Patients**; Jianjun Li [1]; Monika Dzieciatkowska[1]; Xin Liu[1]; Astrid Heikema[2]; Alex van Belkum[2]; Elke Schweda[3]; Michel Gilbert[1]; James C. Richards[1]; *[1]National Research Council, Ottawa, Canada; [2]Erasmus University Medical Center Rotterdam, Rotterdam, The Netherlands; [3]Karolinska Institute, Huddinge, Sweden*

TP 255 **Metaproteomics of Subsurface Microbial Communities in Metal-Contaminated Ecosystems**; Paul Abraham [1]; Nathan C. Verberkmoes[1]; Mark Lefsrud[2]; Karuna Chourey[1]; Manesh Shah[1]; Dawn Holmes[3]; Derek Lovley[3]; Mike Wilkins[4]; Ken Williams[5]; Jill Banfield[4]; Phil Long[6]; Robert Hettich[1]; *[1]Oak Ridge Nat'l Lab, Oak Ridge, TN; [2]Mcgill University, Montreal, Canada; [3]University of Massachusetts, Amherst, MA; [4]University of California, Berkeley, CA; [5]Lawrence Berkeley National Lab, Berkeley, CA; [6]Pacific Northwest National Lab, Richland, WA*

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TP 257 **An Automated, High-Throughput ESI-Mass Spectrometry Assay for the Identification of Enteric Bacterial Pathogens**; Sheri M. Manalili; James C. Hannis; Feng Li; Raymond Ranken; Lawrence Blyn; David J. Ecker; Steven A. Hofstadler; Ranga Sampath; *Ibis Biosciences, Inc., Carlsbad, CA*

TP 258 **Examination of the Protein Complexes Bound on Gal Operon Promoter of Thermoanaerobacter Tengcongensis**; Zhong Qian[1]; Fan Wei[1]; Li Guo[2]; Siqi Liu[1]; *[1]Beijing Genomics Institute, CAS, Beijing, China; [2]Institute of Microbiology, CAS, Beijing, China*

TP 259 **Quantitative Mass Spectrometric Characterization of Substrate-Dependent Changes in the Cellulosome of *Clostridium thermocellum***; Gregory B. Hurst[1]; Chongle Pan[1]; Patricia K. Lankford[1]; Babu Raman[1]; Miguel Rodriguez Jr. [1]; Catherine K. McKeown[1]; Steven D. Brown[1]; Nagiza F. Samatova[2]; Jonathan R. Mielenz[1]; *[1]Oak Ridge National Laboratory, Oak Ridge, TN; [2]North Carolina State University, Raleigh, NC*

TP 260 **Establishment of a Standardized Procedure for Identification of Microorganisms by MALDI TOF Mass Spectrometry**; Thomas Wenzel[1]; Carrie L. Seachord[2]; Thorsten Mieruch[1]; Thomas W. Fuller[3]; Thomas Maier[1]; Richard R. Drake[3]; Markus Kostrzewa[1]; *[1]Bruker Daltonik GmbH, Leipzig, Germany; [2]Children's Hospital of the King's Daughter, Norfolk, VA; [3]Eastern Virginia Medical School, Norfolk, VA*

TP 261 **Imaging MALDI of Bacteria**; David Evason[1]; Hesham Ganbour[2]; Howard Foster[2]; Mark D. Mills[1]; Vic Parr[1]; *[1]SAI, Manchester, UK; [2]Salford University, Salford, UK*

TP 262 **Forensic Microbial Identification Utilizing ESI-TOF Mass Spectrometry**; Raleigh W. Parrott[1]; Kathryn E. O'Brien[1]; Bruce Budowle[2]; James M. Robertson[2]; Steven

A. Hofstadler[3]; Thomas A. Hall[3]; Brian A. Eckenrode[2]; *[1]Oak Ridge Institute for Science and Education, Oak Ridge, TN; [2]Federal Bureau of Investigation, Quantico, VA; [3]Ibis Biosciences, Inc., Carlsbad, CA*

TP 263 **High Resolution Strain Typing of Escherichia coli O157:H7 By MultiLocus PCR Based Mass Spectrometry**; James C. Hannis [1]; Mark W. Eshoo[1]; Feng Li[1]; Thomas A. Hall[1]; David M. Wagner[2]; Lawrence Blyn[1]; Ranga Sampath[2]; Robert E. Mandrell[3]; Clifton K. Fagerquist[3]; Amy Vogler[2]; Paul Keim[2]; Michael Cooley[3]; David J. Ecker[1]; Steven A. Hofstadler[1]; *[1]Ibis Biosciences, Inc., Carlsbad, CA; [2]Northern Arizona University, Flagstaff, AZ; [3]USDA Agricultural Research Service, Albany, CA*

TP 264 **Rapid and Sensitive Identification of Bacterial Antigens by On-Immunoblotted Membrane Digestion**; Akira Okamoto; Keiko Yamada; Michio Ohta; *Nagoya University, Nagoya, Japan*

TP 265 **Comparative Proteomic Analysis of *Aeromonas salmonicida* Grown under Conditions of Salt Stress using Methylation with Isotopically Coded Formaldehydes**; Roger Ebanks; Kenneth Chisholm; Devanand Pinto; *NRC - Institute for Marine Biosciences, Halifax, Canada*

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TP 267 **Quantitative Analysis of a Acyl Coenzyme A in Plant Tissue by LC-MS-MS Electrospray Ionization Method**; Ann Perera; Suh-Yeon Choi; Wuterle Eve; Basil Nikolau; *Iowa State Uiversity, Ames, IA*

TP 268 **Characterization of Ge(IV) and Ni(II) Complexes with Amino Acids using Ion Trap and QqTOF Electrospray Ionization Tandem Mass Spectrometry**; Robert Jirasko; Michal Holcapek; Lenka Kolarova; *University of Pardubice, Pardubice, Czech Republic*

TP 269 **A Rapid and Sensitive Method for the Detection of Residual Biocidal Compounds in Catheter Rinse Solutions by HILIC-MS-MS**; John W. Torchia; Katrina Emilia Nizzi; Bruce Solomon; *Bioanalytical Systems, Inc., West Lafayette, IN*

TP 270 **Analysis of Cellular Free Thiol Amino Acids and Peptides by Stable Isotope Dilution LC-MS**; Stefanie Khartulyari; Cong Wei; Alexander S. Whitehead; Ian A. Blair; *Center for Excellence in Environmental Toxicology, Philadelphia, PA*

TP 271 **Quantitation of Gamma-Aminobutyric Acid in Cerebrospinal Fluid by LC-MS-MS Approach**; Farzin Gharahdaghi; Gennady Smagin; *AstraZeneca, Wilmington, DE*

TP 272 **A New Approach for Highly Sensitive Quantitative LC-MS-MS Analysis of N-Nitrosonornicotine**; Richard Olsen; Kirk Newland; Veni Lapko; *MDS Pharma Services, Lincoln, NE*

TP 273 **LSIMS as a Tool to Study Metal-Complexes of Fullereno-Porphyrins**; Thomas Mueller; Srinivas Banala; Bernhard Kraeutler; *University of Innsbruck, Innsbruck, Austria*

TP 274 **Identification of Biomarkers to Oestrogen Exposure using MCF-7 BOS Cell Line Exposed to 17 Beta-Oestradiol;** Mike Collodoro; Pascale Lemaire; Virginie Bertrand; Rowan L. Dobson; Gabriel Mazzucchelli; Joelle Widart; Edwin De Pauw; Marie-Claire Gillet; *Liege University, Liege, Belgium*

TP 275 **Development of a Sensitive Ultra-Performance LC-MS-MS Method for the Determination of Endogenous Corticosterone in Rat Plasma and Urine**; Yi Tao; Celia D'Arienzo; Hollie Booth; Zheng Ouyang; Timothy Olah; *Bristol Myers Squibb Co., Lawrenceville, NJ*

TP 276 **A Robust LC-MS-MS Method for Analysis of Caffeine and its Metabolite – Paraxanthine in Human Plasma**; Zhilong Gong; Zhilong Gong; *Covance Bioanalytical Svc, Indianapolis, IN*

TP 277 **Mercapturic Acid Conjugates of 4-Hydroxy-2-Nonenal and 4-Oxo-2-nonenal Metabolites in a Rat Model of Oxidative Stress**; Heather C. Kuiper; Cristobal L. Miranda; John Sowell; Jan F. Stevens; *Oregon State University, Corvallis, OR*

TP 278 **Determination of Double Bond Location in Fatty Acids by Manganese Adduction and Electron Induced Dissociation**; Hyun Ju Yoo; Kristina Hakansson; *University of Michigan, Ann Arbor, MI*

TP 279 **Collision Induced Decomposition Pathways of Biliary 4,4'-Methylenedianiline Conjugates Produced in Rats**; Kan Chen[1]; Tammy R. Dugas[2]; Richard B. Cole [1]; *[1]University of New Orleans, New Orleans, LA; [2]LSU Health Sciences Center, Shreveport, LA*

TP 280 **Serum Levels of Isoflavones in Women Receiving a Red Clover Dietary Supplement**; Linlin Dong[1]; Dejan Nikolic[1]; Wenzhong Liang[1]; Suzanne Banuvar[2]; Lee Shulman[2]; Stacie E. Geller[3]; Norman R. Farnsworth[1]; Richard B. Van Breemen[1]; *[1]University of Illinois College of Pharmacy, Chicago, IL; [2]Northwestern University FeinbergSchool of Medicine, Chicago, IL; [3]University of Illinois College of Medicine, Chicago, IL*

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TP 282 **Development and Validation of an Inductively Coupled Plasma Mass Spectrometric Method for the Quantitation of Total Platinum from Oxaliplatin;** Amy Lapaglia; Paula Lee; *ABC Laboratories, Inc., Columbia, MO*

TP 283 **Development of a Highly Sensitive UPLC-MS-MS Method for Quantitative Analysis of CAPE and FCAPE in Rat Plasma;** Jihai Pang; *M.D. Anderson Cancer Center, Houston, TX*

TP 284 **Rapid Method for the Quantitative Determination of Tricin in Human and Rat Plasma using LC-MS-MS**; Gregory Gorman[1]; Lori Coward[1]; Corenna Kerstner-Wood[1]; Lea Freeman[1]; Charles Hebert[1]; Izet Kapetanovic[2]; *[1]Southern Research Institute, Birmingham, AL; [2]National Cancer Institute, Bethesda, MD*

TP 285 **Monitoring of Endogenous Interferences by LC-MS-MS and UV/Vis Spectroscopy: Application to the Determination of Albuterol in Human Plasma**; BRYAN VINING; James Havel; David A Kuntz; Billy G. Hudson; *CRL, Lenexa, KS*

TP 286 **A Sensitive, High-Throughput Method for the Quantitation of Theophylline in Human Plasma via**

Solid Phase Purification and LC-MS-MS Detection; Sarah K. Roby; Yousef J. Basir; Kirk E. Newland; *MDS Pharma Services, Lincoln, NE*

TP 287 **High-Throughput Analysis of Mifepristone and Two Mifepristone Analogues in Mouse Heparin Plasma by LDTD-MS-MS in 9 seconds;** Philippe Nobert[2]; Patrice Tremblay[2]; Sylvain Letarte[1]; Pierre Picard[2]; *[1]Phytronix Technologies, Blainville, Canada; [2]Phytronix Technologies, Inc., Quebec, QC*

TP 288 **A Highly Sensitive LC-MS-MS Method for Quantification of a Pan-erbB kinase Inhibitor-Pd168393 in Plasma**; Jeevan Prasain; Alireza Arabshahi; Ray Moore; Stephen Barnes; Steve Carroll; *University of Alabama at Birmingham, Birmingham, AL*

TP 289 **Determination of Endocannabinoid Antagonist Rimonabant (SR141716) in Plasma by LC-ESI-MS-MS**; Melissa A Mcculloch[1]; Xiang Zhou[1]; Yan Xu[1]; Steve Brunell[2]; Linda Spear[2]; *[1]Cleveland State University, Cleveland, OH; [2]Binghamton University, Binghamton, NY*

TP 290 **Chiral Chromatographic Method Development and Validation for the Quantitation of Eszopiclone in Human Plasma using LC-MS-MS**; Min Meng[1]; Lisa Rohde[1]; Vladimir Capka[2]; Patrick Bennett[1]; *[1]Tandem Labs, Salt Lake City, UT; [2]Astra Zeneca Pharmaceuticals LP, Waltham, MA*

TP 291 **Stable-Isotope Dilution Liquid Chromatography-Tandem Mass Spectrometry Assay for the Quantification of Testosterone in Human Plasma in Diagnosis of Androgen-Mediated Diseases**; Xueheng Zhao; Kenneth D. R. Setchell; *Cincinnati Children's Hospital Medical Center, Cincinnati, OH*

TP 292 **Difficulties in Developing a Sensitive Assay for the Quantification of Rifampin in Multiple Biological Matrices by LC-MS-MS**; Keith Zientek; Michael Nelson; Lori Payne; *BASi, McMinnville, OR*

TP 293 **Stable Isotope Dilution LC-MS Analysis and Biological Relevance of 15-oxo-ETE, A Novel 15-lipoxygenase-Derived Arachidonic Acid Metabolite**; Cong Wei [1]; Peijuan Zhu[2]; Sumit Shah[1]; Ian A. Blair[1]; *[1]Center For Cancer Pharmacology, University of Penn, Philadelphia, PA; [2]Schering Plough, Clark, NJ*

TP 294 **Simultaneous Determination of Loratadine and Betamethasone in Human Plasma using Liquid-Liquid Extraction and High-Performance Liquid Chromatography Coupled to Mass Spectrometry;** Rafael E. Barrientos-Astigarraga; Paulo A. R. Galvinas; Jane K. Finzi; Mauricio R. M. Sampaio; Washington M. Silva; Leandro S. C. Barbosa; *MAGABI Pesquisas Clinicas Farmaceuticas Ltda., Sao Paulo, Brazil*

TP 295 **LC-MS-MS Assay Development and Validation for Determination of Total Doxorubicin (Free + Liposomal) in Human Plasma and Clinical Sample Analysis**; Chaoran Ron Huang[1]; Arnaldo Costa[1]; Dale F. Schoener[2]; Seema Datta[2]; Joseph Whitson[2]; Michael Buonarati[2]; Liyu Yang[1]; *[1]Biogen Idec, Cambridge, MA; [2]Alta Analytical Laboratory, El Dorado Hills, CA*

TP 296 **A Rapid and Sensitive SPE-UPLC-MS-MS Method for Determination of Ropinirole in Human Plasma**; Erin E. Chambers; Diane Diehl; *Waters Corporation, Milford, MA*

TP 297 **Effect of Lycopene on Plasma Testosterone Levels in Men as a Prostate Cancer Prevention Agent**; Ang Liu; Linlin Dong; Richard B. Van Breemen; *University of Illinois College of Pharmacy, Chicago, IL*

TP 298 **Resolving Apparent LC-MS-MS Matrix Effects in Plasma Protein Binding Analysis**; Garnet McRae; Miles Webb; Rahul Vohra; *Painceptor Pharma Corp., Ottawa, Canada*

TP 299 **A Selective LC-MS-MS Method for Quantification of Ribavirin in Human Plasma**; Dawei Zhou; Karla Arriola; Xinping Fang; Jinn Wu; *Xenobiotic Laboratories, Inc., Plainsboro, NJ*

TP 300 **A Highly Sensitive LC-MS-MS Method (0.4 pg/mL) for Quantitation of Formoterol in Human Plasma**; Dawei Zhou; Wenzhong Liang; Xinping Fang; Jinn Wu; *Xenobiotic Laboratories, Inc., Plainsboro, NJ*

TP 301 **Fast Quantitation of Buprenorphine in Human Plasma by MALDI-QqQ$_{LIT}$ using Disposable Matrix Pre-Coated MALDI Plates**; Emmanuel Varesio[1]; Chantal Grivet[1]; Christoph Menzel[2]; Udo Roth[2]; Gérard Hopfgartner[1]; *[1]University of Geneva, Geneva, Switzerland; [2]Qiagen, Hilden, Germany*

TP 302 **Evaluation of Acyl Glucuronide Metabolites during Drug Quantification in Bioanalysis by LC-MS-MS: From Sample Collection to Autosampler Stability;** Melanie Bergeron; Jean-Nicholas Mess; Milton Furtado; Troy Bradley; Fabio Garofolo; *Algorithme Pharma Inc., Laval (Montreal), QC, CANADA*

TP 303 **Bioanalytical Quantitation of Roxithromycin in Human Plasma K3EDTA by LC-MS-MS**; Hassan Rashidzadeh; Yun Chen; Toni Jean Thompson; *Charles River Laboratories, Shrewsbury, MA*

TP 304 **Strategies in Method Development and Determination of Endogenous Vitamin-D3 in Human Plasma by Atmospheric Chemical Ionization Liquid Chromatography/Tandem Mass Spectrometry**; Xuejun Peng; Rong Yi; Amara Pinnawala; Sarah Ostonal; Eliot Chung; Grace van der Gugten; David Gray; *Can Test Ltd, Burnaby, CANADA*

TP 305 **Simultaneous Quantitation of Cytarabine and Uracil Arabinofuranoside in Human Plasma using LC-MS-MS**; Laixin Wang; Yanhui Zhang; Roger Demers; Min Meng; Patrick Bennett; *Tandem Labs, Salt Lake City, UT*

TP 306 **High Throughput and Simultaneously Quantitative Analysis of Selegiline and Three Metabolites in Human Plasma by LC-APCI-Tandem Mass Spectrometry**; Jiongwei Pan[1]; Xiang-yu Jiang[2]; Qin Ji[3]; *[1]Covance, Madison, WI; [2]Covance - 08, Waunakee, WI; [3]Covance , Bioanalytical Chemistry, Madison, WI*

TP 307 **Development of a High Throughput Method for the Quantification of Cholecalciferol in Human Plasma with Deriviatization and LC-MS-MS Detection**; Lee Winchester; Anthony Podany; Corey Ohnmacht; Wei Sun; Chad Briscoe; *MDS Pharma Services, Lincoln, NE*

TP 308 **A Rapid and Highly Sensitive LC-MS-MS Method (10 pg/mL) for Quantitation of Budesonide in Human Plasma**; Guangchun Zhou; Dawei Zhou; Xinping Fang; Jinn Wu; *Xenobiotic Laboratories, Inc., Plainsboro, NJ*

TP 309 **LC-MS-MS Analysis of Aminoglycoside Drugs, Amikacin, Spectinomycin, Streptomycin and Gentamycin, the Challenges and Solutions**; Qi (Angela) Shen[1]; Xin Zhang[1]; Tuyen Nguyen[2]; *[1]Tandem Labs New England, Woburn, MA; [2]Sepracor Inc. 84 Waterford Drive, Marlborough, MA*

TP 310 **Evaluation of Free and Protein-Bound 3-Nitrotyrosine in Human Plasma by Isotope Dilution LC-QqQ with an Artifactual Nitration-Free Proteolysis**; Thierry Delatour; Aurélien Desmarchelier;

Janique Richoz; Christophe Cavin; *Nestle Research Center, Lausanne, Switzerland*

TP 311 **Challenges in Quantitating Low Picogram/mL Levels of Endogenous Compounds;** Kathy Jo Champion[1]; Matthew W. Chapple[1]; Ted Green[1]; George Hade[1]; John R. Perkins[1]; Margret Thorsteinsdottir[2]; *[1]Advion Biosciences, Ithaca, NY; [2]Decode, Reykjavik, Iceland*

TP 312 **Simple and Rapid LC-MS-MS Method to Analyze Anti-Tuberculosis Drugs Ethambutol and Pyrazinamide in Human Plasma**; Yousef Basir; Zhilong Gong; *Covance Bioanalytical, Indianapolis, IN*

TP 313 **Method Development for Measuring 5-Hydroxyindole-3-Acetic Acid in Human Plasma using Liquid Chromatography Tandem Mass Spectrometry**; Changyu Quang; Theodore Brus; Melanie McCort-Tipton; Qin Ji; *Covance, Indianapolis, IN*

TP 314 **Development and Validation of an Improved LC-MS Method to Quantitate Vitamins A, D, and K in a Complex Mixture;** Esther Hwang; Svetlana Zelechonok; Samantha Leidner; Paul M. Bigwarfe Jr.; *Hospira, Inc., Lake Forest, IL*

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TP 315 ***In vitro* Metabolism of LY-320135, a Novel Inverse Agonist for Cannabinoid Receptor (CB1)**; Qiang Zhang; Peng Ma; Guangdi Wang; *Xavier University of Louisia, New Orleans, LA*

TP 316 **Small Molecules and Metabolites Analysis by LC-MS in Plasma using Polymer-Based Internal Surface Reversed Phase Column**; Junji Sasuga[1]; Kei Oide[1]; Eiji Kagawa[1]; Hideyuki Kondo[1]; Yuichi Fusho[2]; Ken Tseng[2]; *[1]Showa Denko, KK, Kawasaki, Japan; [2]Shodex, New York, NY*

TP 317 **Metabolite Identification of Precision-Deuterated Linezolid**; Changfu Cheng; Gary Bridson; Art Morales; David Wells; *Concert Pharmaceuticals, Lexington, MA*

TP 318 **GC-MS Analysis of Human Breath as a Method for Determining Chemical Exposure and Monitoring Human Uptake and Clearance Rates**; Audrey N. Martin[1]; George R. Farquar[1]; A. Daniel Jones[2]; Matthias Frank[1]; *[1]Lawrence Livermore National Laboratory, Livermore, CA; [2]Michigan State University, East Lansing, MI*

TP 319 **LC-MS Detection of Bisphosphonates in Equine Urine and Plasma and Application to an Administration Study of Tiludronic Acid in Horse**; April S Y Wong[1]; Emmie N M Ho[1]; Terence S M Wan[1]; Colton H F Wong[1]; Kenneth K H Lam[2]; Brian D Stewart[2]; *[1]Racing Laboratory, The Hong Kong Jockey Club, Shatin Racecourse, Shatin, N.T., Hong Kong; [2]Veterinary Regulation & International Liaison, Shatin Racecourse, Shatin, N.T., Hong Kong*

TP 320 **Hardware and Software Design Strategies for the Rapid Determination of Optimal Quantitative MS-MS Conditions;** April Smith[1]; Anthony Romanelli[1]; Elliott Jones[1]; John Janiszewski[2]; Hua-fen Liu[1]; Steve Ainley[3]; Richard Schneider[2]; Kevin Shirey[3]; Eva Duchoslav[1]; Loren Olson[1]; *[1]Applied Biosystems, San Jose, CA; [2]Pfizer Inc., Westerly, RI; [3]Sound Analytics, East Lyme, CT*

TP 321 **Study of RNA and Aminoglycoside Complex Binding Properties by ESI-MS-MS**; Keling Dong; Jeffrey Miller; Matthew Willetts; Christie L Hunter; *Applied Biosystems, Framingham, MA*

TP 322 **Evaluation of Immobilized Liquid Extraction to Minimize Ion Supression for LC-MS Analysis of Drugs in Physiological Fluids**; Kerry Nugent [1]; Yixin Zhu[1]; Robert Woleb[2]; *[1]Michrom Bioresources, Inc., Auburn, CA; [2]ILE, Inc., Ferndale, CA*

TP 323 **Investigation of Ultra-High Clearance in Rat for an Inhaled Drug**; Bruce R Heyde; Yiding Hu; Faith Hartsfield; Steve P Wene; Lesley A Albin; *Pfizer, Chesterfield, MO*

TP 324 **Advanced HPLC-MS-MS Methods for Quantitation of Nucleotide and Nucleoside HIV Reverse Transcriptase Inhibitor Metabolites**; Zsuzsanna Kuklenyik; Amy Martin; Chou-Pong Pau; Gerardo Garcia-Lerma; Walid Heneine; John Barr; *Centers for Disease Control and Prevention, Atlanta, GA*

TP 325 **Application of ESI-LC-MS-MS to Mouse Pharmacokinetic Studies using Serial and Parallel Sampling Techniques**; Kevin Kennedy; Jun Tang; Jill Olson; Yun Xiao; Polina Kazavchinskaya; Kim Stringham; Cheryl Wu; *Cerep, Redmond, WA*

TP 326 **Practical Bioanalytical Approach for Analyzing Dose-Formulations Used in PK Studies**; Andrei Stefanescu; Lucy Hetsco; *Seventh Wave Labs, Chesterfield, MO*

TP 327 **Application of UPLC/Dynamic-Flow RAD/MS for Metabolite Identification and Profiling**; Jie Chen; Jie Chen; *JNJPRD, Raritan, NJ*

TP 328 **Plasma Pharmacokinetics and Metabolism of NSC 644221 (A Small Molecule Inhibitor of the Hypoxic Signaling Pathway) in Mic**e; Lawrence R. Phillips[2]; Christine Bramhall[1]; Mark Creighton-Gutteridge[2]; Kimberly D. Hill[1]; Giovanni Melillo[2]; Sherman Stinson[2]; Melinda G. Hollingshead[2]; [1]SAIC, Frederick, MD; [2]NCI/NIH, Frederick, MD

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TP 329 **Quantitative Determination of A Novel CC-Chemokine Receptor 2 (CCR2) Antagonist in Human Plasma using Liquid Chromatography-Tandem Mass Spectrometry**; Hengchang Song; Xiaohui Xu; *Merck & Co, West Point, PA*

TP 330 **The Quantitative Analysis of Clodronate in Human Plasma by Liquid Chromatography/Tandem Mass Spectrmetry**; Wen-Ying Huang; Chin-Hsiung Wang; Yi-Fan Shieh; Shu-Hui Yang; Cheng-Chin Chang; Wen-Lin Wu; *Protech Pharmaservices Corporation, Taipei, Taiwan*

TP 331 **Method Development and Validation for the HPLC-MS-MS Bioanalysis of Vancomycin Extracted from Rat Plasma**; Matthew Pollard; Shane Needham; Chad Christianson; *Alturas Analytics, Inc., Moscow, ID*

TP 332 **Bioanalytical Cross Validation: A Best Practice;** William Bullen [1]; David Muirhead[2]; Trevor Smart[2]; *[1]Pfizer, New London, CT; [2]Pfizer, Sandwich, UK*

TP 333 **Determination of AMP, ADP and ATP using Capillary Ion-Pairing LC-MS-MS**; Jin Ren; Zaichuan Mi; EK Jackson; *University of Pittsburgh, Pittsburgh, PA*

TP 334 **Development of a Bioanalytical LC-MS-MS Assay for the Quantitative Analysis of Amikacin, Neomycin and Gentamicin in Plasma and Tissue**; Jennifer Zimmer[1]; Shane Needham[1]; Jenny McKinnell[2]; Robert Cass[2]; Dane Karr[2]; *[1]Alturas Analytics, Inc., Moscow, ID; [2]Achaogen, South San Francisco, CA*

TP 335 **An Ultrasensitive LC-MS-MS Method for the Quantitation of 6-ß-Naltrexol in Human Plasma using Peak Summing**; Erica Nachi; Ginny B. James; Chris Kafonek; Curtis Sheldon; Chad Briscoe; *MDS Pharma Services, Lincoln, NE*

TUESDAY POSTERS

TP 336 **Validated LC-MS-MS Method for the Quantitative Analysis of the Endocannabinoid Anandamide and Other Ethanolamides in Human Plasma**; Joe Palandra; Jenny Zhang; Jeff Prusakiewicz; Timothy G Heath; *Pfizer, Chesterfield, MO*

TP 337 **Quantitative Analysis of Taurocholate using Ultra-Performance Liquid Chromatography-Tandem Mass Spectrometry**; Amy Q Wang; Hong Cao; Erin D Hugger; Charles B Davis; Charles F McHugh; *DMPK, Oncology CEDD, GlaxoSmithKline, Collegeville, PA*

TP 338 **Simultaneous Determination of Oxymorphone and 6ß-Hydroxyoxymorphone with d3-IS in Human Plasma Despite Isotopic Distribution Overlap by Adjusting Transitions in HILIC-MS-MS**; Jing Ke; Michael Xinzhong Zhang; Siriporn Garritt; Qian Liu; Guiyan Chen; Allan Xu; *Keystone Analytical, Inc., North Wales, PA*

TP 339 **Analysis of Tamoxifen and Midazolam in Plasma: Application of a Non-Linear Weighted Least-Squares Regression Model**; Larry Sallans; Ganesh M. Mugundu; Stephen F. Macha; Pankaj B. Desai; *University of Cincinnati, Cincinnati, OH*

TP 340 **LC-MS-MS Quantitative Analysis of Hydrocortisone in Mouse Serum: Comparison of Liquid-Liquid Extraction (LLE) with Supported Liquid Extraction (SLE)**; Shari Wu; Wenkui Li; Tapan Majumdar; Harold T Smith; Francis LS Tse; *Novartis, East Hanover, NJ*

TP 341 **A Sensitive Semi-Automated Method for the Quantification of Dexamethasone in Human Plasma by LC-MS-MS**; Jonathan Rathe; Karl Linderholm; Chris Kafonek; Dale Raines; Curtis Sheldon; Chad Briscoe; *MDS Pharma Services, Lincoln, NE*

TP 342 **Quantitiation of Corticosteroid in Equine Joint Fluid using the 4000 QTRAP™ System**; Lorraine B Anderson[1]; Mary K Boyce[1]; Seijin Park[2]; Erin D Malone[1]; *[1]University of Minnesota, Minneapolis, MN; [2]Seoul National University, Seoul, South Korea*

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TP 343 **Differentiating Regional Variations in Red Wine with Accurate Mass LC-MS Authors: Ravikanth Veluri, Jonathan Wilson, Ray Sanchez, Ali Kettani, Catherine Stacey**; Ravikanth Veluri; *Bruker Daltonics, Burlington, MA*

TP 344 **Phase I and Phase II Metabolite Identification on a Triple-Quadrupole Mass Spectrometer using 2 millisecond Dwell Times**; Allen Zhang[123]; Laurance Lee[123]; Patrick Jeanville[123]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Thermo Fisher Scientific, San Jose, CA; [3]Thermo Fisher Scientific, West Palm Beach, FL*

TP 345 **Identification of Metabolites by Ultra High-Pressure Liquid Chromatography and Data-Dependent Accurate Mass Analysis using LTQ/Orbitrap in Internal Mass Calibration Mode**; Heng-keang Lim; Jose Silva; *Johnson and Johnson PRD, Raritan, NJ*

TP 346 **Automated Software Analysis of Isotope Cluster Mass Differences for Components in LC-MS Datasets**; Graham A. McGibbon[1]; Mark A. Bayliss[1]; Margaret Antler[1]; Vitaly Lashin[2]; *[1]Advanced Chemistry Development Inc., Toronto, ON; [2]ACD, Moscow, Russia*

TP 347 **Metabolic Interspecies Comparison by LC-MS and Principle Component**; Tania A. Sasaki[1]; Robert Cho[2]; Claire Bramwell-german[1]; Elliott Jones[1]; Ji Ma[2]; *[1]Applied Biosystems, Foster City, CA; [2]Amgen Inc., South San Francisco, CA*

TP 348 **An Integrated Approach to Metabolite ID through Combination of Experimental LC-MS Data and In Silico Metabolite and Fragmentation Prediction**; Kim A. Johnson[1]; Vinod K. Arora[1]; W. Griffith Humphreys[2]; Yue-Zhong Shu[1]; *[1]Bristol-Myers Squibb, Wallingford, CT; [2]Bristol- Myers Squibb, Princeton, NJ*

TP 349 **The Benefits of Small Particte Columns with Conventional HPLC Systems for Metabolite Profiling of Radioactive and Non-Radioactive Samples by LC-MS**; Natalia Penner; Zhiling Li; Swapan Chowdhury; *Schering-Plough Res. Inst., Kenilworth, NJ*

TP 350 **Correlation and Convolution Analysis of Accurate Mass Spectrometry Data for Detection of Metabolites**; Eva Duchoslav [2]; Yves G. Leblanc[1]; *[1]MDS Analytical Technologies, Concord, ON; [2]MDS Sciex, Concord, ON*

TP 351 **Metabolite Identification using a Unit Mass Resolution Liquid Chromatography/Mass Spectrometry with Accurate Formula Identification and Mass Defect Filtering**; Mei-yi Zhang [1]; Ming Gu[2]; Natasha Kagan[1]; Anokha Ratnayake[1]; *[1]Wyeth Research, Princeton, NJ; [2]Cerno Bioscience, Danbury, CT*

TP 352 **Identification of Drug Metabolites by UPLC-MS with Isotope Pattern Directed Mass Chromatograms and UPLC with Radioactivity Flow Detection**; William de Maio; Matthew Hoffmann; Michael Carbonaro; Robin Moore; Abdul Mutlib; Rasmy E. Talaat; *Wyeth Research, Philadelphia, PA*

TP 353 **Structural Characterization of *in vitro* Rat Liver Microsomal Metabolites of a Selective Muscarinic M_2 Receptor Antagonist using LTQ-Orbitrap Mass Spectrometer**; Guodong Chen; Ibrahim Daaro; Joseph Kozlowski; Birendra N. Pramanik; *Schering-Plough Research Inst., Kenilworth, NJ*

TP 354 **High Resolution Metabolite Identification for Lafutidine in Rat Urine by UPLC/oa-TOF MS**; Kate Yu [1]; Jose Castro-perez[1]; John P. Shockcor[1]; Yuya Wang[2]; Xiaoyan Chen[2]; Dafang Zhong[2]; *[1]Waters Corporation, Milford, MA; [2]Chinese Academy of Science, Shanghai, China*

TP 355 **Rapid Metabolic Stability Screening with Simultaneous Metabolite Profiling Studies of Clozapine in Rat Hepatocytes**; Yingbo Yang; Ru Qiu (Sophie) Pan; Concettina Catalano; Julia Izhakova; Douglas J. Turk; *NoAb BioDiscoveries Inc., Mississauga, ON*

TP 356 **Extracting Relevant Data Out of the MS Background**; Filip Cuyckens; Rob Hurkmans; Laurent Leclercq; Russell Mortishire-smith; *Johnson & Johnson Pharma R&D, Beerse, Belgium*

TP 357 **Gender Specific In-Vitro Metabolism Analysis from Tri-Cyclic Antidepressant Drugs by Hybrid Quadrupole Time-of-Flight Mass Spectrometry and Principle Component Software;** Susan Leonard; Johnie Brown; Jeffrey Miller; Elliott Jones; *Applied Biosystems, Framingham, MA*

TP 358 **New Approach for Identification of Metabolites of a Model Drug; Partial Isotope-Enrichment Combined with Novel Mass Spectral Modelling Software;** Richard T. Gallagher[1]; Ian D. Wilson[1]; Kirsten Hobby[2]; *[1]AstraZeneca, Macclesfield, UK; [2]Kisotopic Solutions, Manchester, UK*

TP 359 **Isoscore: Automated Localization of Biotransformations by Mass Spectrometry using Product Ion Scoring of Virtual Regioisomers**; Laurent Leclercq [1]; Russell Mortishire-smith[1]; Maarten

Huisman[1]; Filip Cuyckens[1]; Alastair Hill[2]; Michael Hartshorn[2]; *[1]Johnson & Johnson, Beerse, Belgium; [2]Dotmatics, Bishop Stortford, UK*

TP 360 **Characterization of C- and N-oxidized Clemastine Metabolites using LC-MS^n**; Annica Tevell Åberg[1]; Ulf Bondesson[2]; Mikael Hedeland[2]; *[1]Uppsala University, Uppsala, Sweden; [2]National Veterinary Institute, Uppsala, Sweden*

TP 361 **Evaluation of MS-MS Methods: CID, PQD and HCD in an LTQ-Orbitrap Mass Spectrometer for Structural Elucidation of Metabolites**; Neil Blumenkrantz; Ragu Ramanathan; Swapan Chowdhury; Kevin Alton; *Schering-Plough Research Institute, Kenilworth, NJ*

TP 362 **An Evaluation of Different Scan Functions to Identify Nefazodone Metabolites *in vitro* Samples using a LC-QqQ/LIT Mass Spectrometry**; Daniel Lebre; Gary Impey; Julie Wingate; *Applied Biosystems/MDS Sciex, Concord, Canada*

TP 363 **A Chemically Intelligent Metabolite Identification LC-MS-MS Workflow with a C-Heteroatom Cleavage Tool and Automatic Generation of Mass Defect Filters**; Jeff Goshawk[1]; Kate Yu[1]; Henry Shion[2]; John Shockcor[2]; Jose Castro-Perez[2]; Michael Hartshorn[3]; Alastair Hill[3]; Russell Mortishire-Smith[4]; *[1]Waters MS Technology, Manchester, UK; [2]Waters Corp, Milford, USA; [3]Dotmatics Ltd, Herts, UK; [4]J&J Pharmaceutical R&D, Beerse, Belgium*

TP 364 **Frequently Reported Mass Differences and Formula for List Searching in Drug Metabolite Identification**; Peter L. Jacobs; Lars Ridder; *N.V. Organon, a part of Schering-Plough Corp., Oss, Netherlands*

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TP 365 **Rapid Nontargeted Metabolite Profiling of Cancer Cells Treated with Potential Cancer Therapeutic Agents using Electrospray Ionization Mass Spectrometry**; Ruth N. Udey; Chrysoula Vasileiou; Babak Borhan; A. Daniel Jones; *Michigan State University, East Lansing, MI*

TP 366 **UPLC MS-MS Assay of Jasmonates and Related Phytohormones for Large-Scale Screening of Plant Metabolic Phenotypes**; Xiaoli Gao; Abraham J. K. Koo; Gregg A. Howe; A. Daniel Jones; *Michigan State Unviersity, East Lansing, MI*

TP 367 **LC-MS Multivariate Analysis of Beer for the Discovery of Commercially Important Compounds**; Masahiro Maeda[1]; Hideaki Uchida[1]; Shigeki Araki[2]; Toshiyuki Oshima[2]; Youichi Tsuchiya[2]; Katsuaki Maeda[2]; Junji Watari[2]; Steve Fischer[3]; *[1]Agilent technologies Japan, Tokyo , Japan; [2]Sapporo Breweries Ltd, Shizuoka, Japan; [3]Agilent Technologies, Santa Clara, CA*

TP 368 **Quantitative Profiling of Metabolites of Polyunsaturated Fatty Acids Modulated by Dietary N-3 Deficiency in Rat Lung Tissues by HPLC/ESI-MS-MS**; Jeongrim Lee; Kei Hamazaki; Hee-Yong Kim; *NIH/NIAAA, Rockville, MD*

TP 369 **Visualizing Islet Metabolism by ^{13}C Labeling and Capillary Liquid Chromatography – Nanoelectrospray Ionization Mass Spectrometry (cLC-nESI-MS)**; Qihui Ni; Robert T Kennedy; *University of Michigan, Ann Arbor, MI*

TP 370 **High-Resolution Separation and Identification of Structural Isomers of Endogenous Acylcarnitine Metabolites in Human Urine**; Azeret Zuniga; Liang Li; *University of Alberta, Edmonton, Canada*

TP 371 **Defining Instrument Performance and Assessing the Reproducibility of Mass Spectrometric Analyses of Complex Samples**; Paolo Lecchi; Jean Zhao; Wes Wiggins; Greg Bertenshaw; Tzong-Hao Chen; Brian Mansfield; John M. Peltier; *Correlogic Systems, Inc., Rockville, MD*

TP 372 **Unraveling Control and Regulation in Metabolic Pathways from Quantitative Metabolomics and ^{13}C Metabolic Flux Analysis**; Nicola Zamboni; Jennifer Ewald; Stefan Jol; Anne Kuemmel; Uwe Sauer; Matthias Heinemann; *ETH Zürich, Zürich, Switzerland*

TP 373 **Quantitative Analysis of Bile Acids in Various Biological Fluids using LC-MS-MS Isotopic Dilution Technique**; Philippe A. Guy; Mounir Meknaci; Francois-Pierre Martin; Sunil Kochhar; *Nestlé Research Center, Lausanne, Switzerland*

TP 374 **Metabolomics for Global Assessment of Antioxidant Capacity using Capillary Electrophoresis-Mass Spectrometry**; Richard Lee; Philip Britz-McKibbin; *McMaster University, Hamilton, Canada*

TP 375 **Metabolic Profiling of Endocannabinoids and Related Fatty Acid Amides and Glyceryl Esters in Rat Tissue and Plasma Samples**; Katrin Georgi[1]; John W. Newman[2]; Bruce D. Hammock[1]; *[1]UC Davis, Davis, CA; [2]USDA, ARS, Western Human Nutrition Research Center, Davis, CA*

TP 376 **High Resolution Mass Spectrometry: Quantitative Metabolomic Analysis of Butanol Stress Response in E. coli**; Francesco Pingitore; Aindrila Mukhopadhyay; Jay Keasling; Marcin Joachimiak; *University of California, Berkeley/ LBNL, Berkeley, CA*

TP 377 **Metabolic Profiling of Carnitine, Aminoacids, and Phospholipids-Based Compounds in Plasma Samples by UHPLC and Monolithic HPLC/ESI/APCI-MS;** Estela Soledad Cerutti; Timothy Garrett; Peggy Borum; Jodie V. Johnson; Richard A. Yost; David H. Powell; *University of Florida, Gainesville, FL*

TP 378 **Characterizing Sodium Phenylbutyrate (SPB) Metabolites from Huntington's Disease (HD) Plasma using Parallel LCECA/LC-MS**; Erika N. Ebbel[1]; Susan Schiavo[2]; Lei Wang[3]; Wayne R. Matson[4]; Mikhail B. Bogdanov[3]; Stephen Hersch[5]; Catherine E. Costello[1]; *[1]Boston U School of Medicine, Boston, MA; [2]Northeastern University, Boston, MA; [3]Weill Medical College of Cornell University, New York, NY; [4]Bedford VA Medical Center, Bedford, MA; [5]MA General Hospital, Harvard Medical School, Boston, MA*

TP 379 **Targeted Metabolomics Analysis of Recombinant *Saccharomyces* Strains by Capillary Electrophoresis - Electrospray Mass Spectrometry**; Joseph P.M. Hui[1]; Elizabeth Huenupi[1]; Jan-Maarten Geertman[2]; Theresa C. White[2]; Evelyn C. Soo[1]; *[1]NRC - Institute for Marine Biosciences, Halifax, Canada; [2]Iogen Corporation, Ottawa, Canada*

TP 380 **Comparison of GC-MS and NMR Metabolite Identification in White Wines: Insights into the Chemical Basis for Wine Body**; Kirsten Skogerson[1]; Ron Runnebaum[2]; Oliver Fiehn[1]; *[1]UC Davis Genome Center, Davis, CA; [2]UC Davis, Davis, CA*

TP 381 **Rapid LC-MS-MS Determination of Intermediates Produced during Glycolysis**; Keri Ross; Joseph J. Dalluge; *Cargill Incorporated, Excelsior, MN*

TP 382 **A Metabolomic Screening and Quantification of Hexose Monophosphates for Neonatal Galactosemia in Whole Blood using Electrospray Tandem Mass Spectrometry (ESI/MS-MS)**; Sung Hyun Hong; Hae-

Ran Moon; *Specialty Lab Solution, Suwon, Gyeonggi-Do, South Korea*

TP 383 **Image-Based Differential Mass Spectrometry Data Analysis for the Discovery of Markers of Liver Toxicity by Metabolomics**; Peter Askovich[1]; Cindy Chepanoske[1]; Andrey Bondarenko[1]; Yutai Li[2]; Kara Pearson[2]; Caroline K Ferraro[2]; Amy F. Loughlin[2]; Ethan Xu[2]; William H. Schaefer[2]; *[1]Rosetta Biosoftware, Seattle, WA; [2]Merck & Co., Inc, West Point, PA*

TP 384 **Validated Quantitative Metabolic Signature using Gas Chromatography-Mass Spectrometry Based Steroid Analysis**; Ju-Yeon Moon[1]; Man-Ho Choi[1]; Hyun-Jin Jung[1]; Myeong Hee Moon[2]; Bong Chul Chung[1]; *[1]Life Sciences Division / KIST, Seoul, South Korea; [2]Dept. of Chemistry / Yonsei Univ., Seoul, Korea*

TP 385 **Identification of Novel Endogenous Metabolites of Acylglycines in Human Urine**; Avalyn Lewis; *University of Alberta, Edmonton, Canada*

TP 386 **Identifying Biomarkers for Rheumatiod Arthritis in the Human TNF-driven Tg197 Mouse Model using High Mass Accuracy MSn Analysis**; Eleni Gika[2]; Georgios Theodoridis[2]; Neil J Loftus[1]; Ian Wilson[4]; Simon Ashton [1]; Lefteris Zacharia[5]; Yiannis Sotsios[5]; George Kollias[3]; *[1]Shimadzu, Manchester, UK; [2]Aristotle University, Thessaloniki, Greece; [3]Biomedical Sciences Research Center, Vari, Greece; [4]Astra Zeneca, Alderley Edge, UK; [5]Biomedcode Hellas SA, Vari, Greece*

TP 387 **Metabolite Profiling of Single Secretory and Glandular Trichomes of the Genus Solanum using Laser Desorption/Ionization (LDI) Mass Spectrometry and LC-MS**; Chao Li; Feng Shi; A. Daniel Jones; *Michigan State University, East Lansing, MI*

TP 388 **Validated Analytical Method for Quantification and Identification of Coenzyme-A Activated Compounds in Biological Tissues by online SPE-LC-MS-MS**; Christoph Magnes[1]; Maria Suppan[1]; Thomas Pieber[2]; Guenter Haemmerle[3]; Frank Michael Sinner[1]; *[1]Joanneum Research, Inst of Med. Technologies and H, Graz, Austria; [2]Medical University of Graz, Dep. of Int. Medicine, Graz, Austria; [3]University of Graz, Inst. of Molecular Bioscience, Graz, Austria*

TP 389 **The Capacity of the Human Endometrium to Synthesise Steroids: a Metabolomic (Mass Spectrometry) and Genomic (RT-PCR) Approach;** Angela E Taylor; John O White; Gareth Brenton; Deya Gonzalez; Edward Dudley; *Swansea University, Swansea, UK*

TP 390 **A Simple LC-MS-MS Method for Metabolite Profiling of Mevalonate Pathway and Associated Co-Factors in Metabolically Engineered Yeast and Bacteria**; Sunil Bajad; Nathan Moss; Tina Mahatdejul; Sunil Chandran; Michael Leavell; *Amyris Biotech, Emeryville, CA*

TP 391 **Targeted Metabolic Profiling of Heart Failure Mouse Model by Selected-Reaction Monitoring of Fatty Acid Metabolites**; Lekha Sleno; Anthony Gramolini; Andrew Emili; *University of Toronto, Toronto, Canada*

TP 392 **Profiling Bacterial Virulence with Quantitative Metabolomics**; Jan Crowley; John Turk; Scott Hultgren; Jeffrey Henderson; *Washington University School of Medicine, St. Louis, MO*

TP 393 **GC-TOF-MS Based Metabolomics for the Analysis of Plant Biodiversity and Phenytypic Plasticity in a Typical Grassland Community**; Christian Scherling; Wolfram Wweckwerth; *Max-Plank-Institute, Potsdam-Golm, Germany*

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TP 395 **High-Throughput Discovery of Signaling Peptides in the *Aplysia* Central Nervous System**; Fang Xie; Elena Romanova; Jonathan Sweedler; *University of Illinois at Urbana-Champaign, Urbana, IL*

TP 396 **Novel Inactivation Technology Preserves the *in vivo* Levels of Proteins, Peptides and Phosphorylations in Tissue Samples**; Marcus Svensson[1]; Jonas Larsson[1]; Mats Borén[1]; Maria Fälth[2]; Per E. Andren[2]; Per Svenningsson[3]; Karl Sköld[1]; *[1]Denator AB, Gothenburg, Sweden; [2]Uppsala University, Uppsala, Sweden; [3]Karolinska Institutet, Stockholm, Sweden*

TP 397 **Enrichment and Characterization of C-terminally Blocked Neuropeptides in Cancer borealis Brain Tissue**; Xin Wei; Feng Xiang; Mingming Ma; Lingjun Li; *Univ.of Wisconsin-Madison, Madison, WI*

TP 398 **Quantitative Tandem Mass Spectrometry Based Search for Sex-Specific Neuropeptides in Insects**; Peter D. Verhaert [1]; Inez M. Finoulst[1]; Peter Schulz-knappe[2]; Martijn Pinkse[1]; *[1]Delft University of Technology, DELFT, Netherlands; [2]Proteome Sciences R&D Gmbh Co.kg, Frankfurt, Germany*

TP 399 **Mass Spectrometry Reveals Activity Dependent Release of Protein Fragments at the Synapse**; Suresh P Annangudi; Soong Ho Kim; Ivan Jeanne Weiler; Stanislav Rubakhin; William T Greenough; Jonathan V Sweedler; *Beckman Institute, University of Illinois, Urbana, IL*

TP 400 **Comparative Neuropeptidomic Analysis of Food Intake via a Multi-faceted MS Approach**; Ruibing Chen; Stephanie Cape; Junhua Wang; Yuzhuo Zhang; Lingjun Li; *UW, Madison, Madison, WI*

TP 401 **Neuropeptide Characterization in Brain Tissue using Recent Advances in Mass Spectrometry**; A.F. Maarten Altelaar[1]; Shabaz Mohammed[1]; Roger A.H. Adan[2]; Albert J.R. Heck[1]; *[1]Utrecht University, Utrecht, The Netherlands; [2]University Medical Center, Utrecht, The Netherlands*

TP 402 **Mass Spectrometric Investigation of Individual Mammalian Cells Selected via Molecular Biology Markers**; Stanislav S. Rubakhin [1]; Georgina M. Aldridge[2]; William T. Greenough[3]; Jonathan V. Sweedler[4]; *[1]Beckman Institute, UIUC, Urbana, IL; [2]Neuroscience Graduate Program, UIUC, Urbana, IL; [3]Department of Cell and Structural Biology, UIUC, Urbana, IL; [4]Department of Chemistry, UIUC, Urbana, IL*

TP 403 **Mass Spectrometric Characterization of the Crustacean Hyperglycemic Hormone (CHH) in the Sinus Gland of Cancer borealis**; MINGMING MA; Joshua J. Schmidt; Ying Ge; Lingjun Li; *University of Wisconsin---Madison, Madison, WI*

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TP 406 **Peptidomic Analysis of Astrocytes using Liquid Chromatography Coupled to Mass Spectrometry (LC-MS)**; Ping Yin; Ann Knolhoff; Suresh Annangudi; Larry Millett; Martha Gillette; Jonathan Sweedler; *University of Illinois at Urbana-Champaign, Urbana, IL*

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TP 411 **Charge and Functional Group Based Extraction and Detection of Peptides using Dendrimeric Inverse Micelles and MALDI-TOF MS**; Andrea Gomez; Malar Azagarsamy; Sankaran Thayumanavan; Richard Vachet; *University of Massachuset, Amherst, MA*

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TP 414 **Generating Peptide Titration Curves using Polymeric Inverse Micelles and MALDI-MS Analysis**; Nadnudda Rodthongkum; Elamprakash N. Savariar; Ramgopal Mettu; Sankaran Thayumanavan; Richard W. Vachet; *University of Massachusett, Amherst, MA*

TP 415 **Detection of Helix Formation in Gas-Phase Peptides by Fluorescence Measurements of Trapped Ions**; Huihui Yao; Geng Li; Anthony Rullo; Rebecca Jockusch; *Department of Chemistry, University of Toronto, Toronto, Canada*

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TP 421 **Discovery, Sequencing and Chemical Synthesis of a Highly Selective Ligand Binding an Orphan Adrenoreceptor Subtype in the Green Mamba Venom**; Loïc Quinton[1]; Céline Rouget[2]; Gilles Mourier[2]; Robert Thaï[2]; Steven Dubois[2]; Nicolas Gilles[2]; Edwin De Pauw[1]; *[1]University of Liege - Mass Spectrometry Laboratory, Liege, Belgium; [2]CEA Saclay, DSV/iBiTec-S/SIMOPRO, Gif-sur-Yvette, France*

TP 422 **The Contribution of Ammonium Sulfate and In-Source Decay in Peptides Sequencing;** Alice Delvolvé; Amina S. Woods; *NIH/NIDA/IRP, Baltimore, MD*

TP 423 **Application of Electron Transfer Dissociation in Peptidomic Analysis**; Junko Kimata[1]; Kazuki Sasaki[2]; *[1]Thermo Fisher Scientific, Osaka, Japan; [2]National Cardiovascular Center, Osaka, Japan*

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TP 430 **Selective Derivatization of Cysteines for the Enhancement of UV Photodissociation of Peptides**; Lisa A Vasicek[1]; Jennifer Brodbelt[2]; *[1]University of Texas, Austin, TX; [2]The University of Texas, Austin, TX*

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TP 433 **Aspartocin Antibiotic Complex A, B & C: Structure Characterization by ESI-MS-MS and ESI-Nozzle-Skimmer-MS-MS**; Marshall M. Siegel; Fangming Kong; Xidong Feng; Guy Carter; *Wyeth Research, Pearl River, NY*

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TP 437 **Elimination of Six Human Phospholipids with Downfield Suppression Potential from Protein Precipitation Extracts using a Novel Phospholipid Scavenger Plate;** Mary Pelzer[1]; Hongliang Jiang[2]; Qin Ji[3]; An Trinh[4]; *[1]Covance, Madison, WI; [2]Covance Laboratories Inc., Madison, WI; [3]Covance , Bioanalytical Chemistry, Madison, WI; [4]Sigma-Aldrich, St. Louis, MO*

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TP 458 **MALDI TOF/TOF Is a Convenient Tool for the Identification and Quantification of Multiply Phosphorylated Peptides from Low Complexity Samples**; Andreas Schmidt[4]; Goran Mitulovic[2]; Edina Csaszar[3]; Gustav Ammerer[3]; Karl Mechtler[1]; *[1]IMP Research Institute of Mo, Vienna, Austria; [2]Imba Inst. of Mol. Biotech., Vienna, Austria; [3]Max F. Perutz Laboratories, Vienna, Austria; [4]Cd Laboratory / Vienna, Vienna, Austria*

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TP 467 **Study of Acetylated Lysine, Serine, Threonine, and Tri-Methylated Lysine Containing Peptides using Electrospray Collision-Induced Dissociation Tandem Mass Spectrometry**; Yan Li; Haydn Ball; *UTSW, Dallas, TX*

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TP 476 **Identification of Ubiquitination Sites on MHC-I Molecules by Mass Spectrometry**; Stephen Swatkoski[1]; Xiaoli Wang[2]; Ted Hansen[2]; Robert Cotter[1]; *[1]Johns Hopkins University School of Medicine, Baltimore, MD; [2]Washington University School of Medicine, St. Louis , MO*

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TP 481 **CA11, An Autocrine Protein in Gastric Epithelium, Plays a Role in Regulation of Cell Cycle**; Rui Xing[1]; Jun Zhang[1]; Bin Kang[1]; Siqi Liu[1]; Youyong Lu[2]; *[1]Beijing Genomics Institute, CAS, Beijing, China; [2]Peking University, School of Oncology, Beijing, China*

TP 482 **Proteomics Approach to Identify the Components of Huntingtin Aggresome Machinery and Exploration of the Molecular Mechanisms Leading to Aggresome Formation**; Yan Wang; Anatoli B. Meriin; Michael Y. Sherman; Catherine E. Costello; *Boston University School of Medicine, Boston, MA*

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TP 484 **Charge State Dependent Fragmentation of Gaseous Alpha-Synuclein Ions via Ion Trap CID, Beam-Type CID, and ETD**; Chamnongsak Chanthamontri; Jian Liu; Scott A. Mcluckey; *Purdue University, West Lafayette, IN*

TP 485 **Identification of Binding Partners of hDSS1 using MALDI and LC-ESI Based Mass Spectrometry**; Sung-Jen Wei[1]; Katina Johnson [1]; Hong Dang[2]; Thomas Darden[1]; Bryan Betz[1]; Margaret Humble[1]; Carol Trempus[1]; Jason Williams[1]; Ronald Cannon[1]; Raymond Tennant[1]; *[1]NIEHS/NIH/DHHS, Research Triangle Park, NC; [2]Alpha-Gamma Technologies Inc., Raleigh, NC*

TP 486 **Peptide Products of Vsca1 and hSMR3A as Markers for Erectile Dysfunction (ED) in Diabetic and Non-Diabetic Etiolgies;** Giridharan Gokulrangan[1]; Jinsook Chang[1]; Janna Kiselar[1]; Kelvin Davies[2]; Mark Chance[1]; *[1]Case Proteomics Center, Cleveland, OH; [2]Albert Einstein Colege of Medicine, Cleveland, OH*

TP 487 **Protein Microheterogeneity and the Need for Population Proteomics for Protein Characterization: Case Study of Vitamin D Binding Protein**; Chad R. Borges; Jason W. Jarvis; Paul E. Oran; Stephen P. Rogers; Randall Nelson; *Arizona State University, Tempe, AZ*

TP 488 **Total de novo Sequencing of Myelin P2 and Identification of its Lipid Ligand**; Gianluca Maddalo[1]; Mohammadreza Shariatgorji[1]; Chris Adams[2]; Eva Fung[2]; Jan Sedzik[3]; Ulrika Nilsson[1]; Roman Zubarev[2]; Leopold L. Ilag[1]; *[1]Stockholm University, Stockholm, Sweden; [2]Uppsala University, Uppsala, Sweden; [3]Karolinska Institute, Stockholm, Sweden*

TP 489 **Characterization of the Der4 Multiprotein Complex for the Elucidation of its Role in Acute Lymphoblastic Leukemia (ALL)**; Sabrina Baltruschat; Anne Benedikt; Adelheid Bursen; Tabiwang Arrey; Björn Meyer; Rolf Marschalek; Michael Karas; *Johann Wolfgang Goethe-University, Frankfurt, Germany*

TP 490 **Identification and Characterization of Structural Proteins in the Complex Phage 201phi2-1 by Mass Spectrometry**; Susan T. Weintraub; Julie A. Thomas; Mandy Rolando; Stephen C. Hardies; Philip Serwer; *University of Texas HSC, San Antonio, TX*

TP 491 **Characterization of Intact Complexes of Anticancer Drugs and Serum Proteins, Enzymes and Antibodies using Electrospray Mass Spectrometry**; Sool Yeon Cho; James F. Holland; John Roboz; *Mount Sinai School of Medicine, New York, NY*

TP 492 **Exploring the Functional Roles of BAG2 in Senescence with Identification of its Interaction Complexes**; Ju Zhang[1]; Xiaomin Lou[1]; Shangbin Yang[2]; Siqi Liu[1]; Ningzhi Xu[1]; *[1]Beijing Genomics Institute, CAS, Beijing, China; [2]Cancer Institute, CAMS, Beijing, China*

TP 493 **A Detailed Characterisation of the Interaction between the PEBP/RKIP Protein and Locostatin, a Potential Antimetastatic Lead**; Guillaume Gabant[1]; Martine Beaufour[1]; Françoise Schoentgen[2]; Martine Cadene[1]; *[1]CBM CNRS, Orleans, FRANCE; [2]IMPMC CNRS, Paris, France*

TP 494 **Characterization of a Novel Subunit of the Drosophila Melanogaster Chromatin Remodeling Complex PBAP**; Gillian E Chalkley[1]; Yuri M Moshkin[1]; Karin Langenberg[1]; Karel Bezstarosti[1]; Andras Blastyak[2]; Henrik Gyurkovics[2]; Jeroen AA Demmers [1]; C. Peter Verrijzer[1]; *[1]Erasmus Medical Center, Rotterdam, Netherlands; [2]Hungarian Academy of Sciences, Szeged, Hungary*

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TP 495 **Limited Proteolysis and Oxidative Surface Mapping for Characterization of the DNA-Binding Domain of Mismatch Repair Protein Pms1 by Mass Spectrometry**; Allison N Schorzman[1]; Jenny M Cutalo[2]; Lars C Pedersen[1]; Thomas A Kunkel[1]; Kenneth B. Tomer[1]; *[1]NIEHS, Research Triangle Park, NC; [2]Federal Bureau of Investigation, Quantico, VA*

TP 496 **Conformational Studies of a Monoclonal Antibody, IgG1, by Chemical Oxidation: Structural Analysis by Ultra Performance LC-ESI-ToFMS and Multivariate Data Analysis**; Leila Zamani[1]; Fredrik O. Andersson[2]; Yang Yang[2]; Per Edebrink[2]; Sven P. Jacobsson[2]; *[1]Stockholm University, Stockholm, Sweden; [2]AstraZeneca, Södertälje, Sweden*

TP 497 **Experimental and Informatic Aspects of Electrochemical Oxidation as a Surface Mapping Probe for Higher Order Protein Structure**; Carlee McClintock; Vilmos Kertesz; Susie Dai; Robert Hettich; *Oak Ridge National Laboratory, Oak Ridge, TN*

TP 498 **FPOP Labels Proteins Faster than they Unfold;** Brian C. Gau [1]; Joshua S. Sharp[2]; Don L. Rempel[1]; Michael L. Gross[1]; *[1]Washington University, St. Louis, MO; [2]University of Georgia, Athens, GA*

TP 499 **Monitoring Conformational Changes of the Bacillus anthracis Protective Antigen with Differential Oxidative Surface Mapping**; James G. Smedley, III[1]; Joshua S. Sharp[2]; Jeffrey F. Kuhn[3]; Kenneth B. Tomer[1]; *[1]NIEHS, Durham, NC; [2]University of Georgia, Athens, GA; [3]Varian Analytical Instrum, Cary, NC*

TP 500 **Use of Oxidation and Mass Spectrometry to Elucidate the Function Mechanism of a DNA-Architecture Protein**; Françoise Culard; Corinne Bure; Melanie Spotheim; Martine Cadene; *CBM du CNRS, Orleans, FRANCE*

TP 501 **Probing the Structure of Short-Lived Protein Folding Intermediates by Hydroxyl-Radical-Mediated Oxidative Labeling and ESI-MS**; Bradley B. Stocks; Lars Konermann; *Univ. of Western Ontario, London, ON*

TP 502 **Substrate Binding Inhibits Chemical Modification of Human Bile Acid CoA:Amino Acid N-acyltransferase**

(hBAT); Erin M Shonsey; Stephen Barnes; Matthew B Renfrow; *UAB, Birmingham, AL*

TP 503 **Structural Characterization of the Calcium Binding Protein Calbindin-D28k**; Carey A. Hobbs[1]; Leesa J. Deterding[2]; Richele J. Thompson[1]; Benjamin G. Bobay[1]; Kenneth Tomer[2]; John Cavanagh[1]; *[1]North Carolina State University, Raleigh, NC; [2]NIEHS, Research Triangle Park, NC*

TP 504 **Protein Surface Mapping by Employing Hydroxyl Radicals, Mass Spectrometry and Molecular Dynamics Simulations**; Olga Charvatova[1]; B. Lachele Foley[1]; Marshall W. Bern[2]; Joshua S. Sharp[1]; Ron Orlando[1]; Robert J. Woods[1]; *[1]University of Georgia, Athens, GA; [2]Palo Alto Research Center, Palo Alto, CA*

TP 505 **Surface Mapping of β-2-Microglobulin Oligomers using Covalent Labeling and Top-down Sequencing**; Mark Olbris; Vanessa Leah Mendoza; Richard Vachet; *University of Massachusetts, Amherst, MA*

TP 506 **Probing the Structure of Serpin/Protease Complexes by Structural Mass Spectrometry Method**; Xiaojing Zheng; Patrick Wintrode; Mark Chance; *Case Western Reserve Univ, Cleveland, OH*

TP 507 **Combining Structural Mass Spectrometry and Rosetta: Experimental Data Constrained de novo Structure Inference**; Keiji Takamoto[1]; Xiaojing Zheng[1]; Janna Kiselar[1]; Rhiju Das[2]; Robert Vernon[2]; David Baker[2]; Mark Chance[1]; *[1]Case Western Reserve University, Cleveland, OH; [2]University of Washington, Seattle, WA*

TP 508 **Pulsed Electron Beam Water Radiolysis: A Novel Method for Sub-Microsecond Hydroxyl Radical Protein Footprinting**; Caroline Watson[1]; Deanna O'Donnell[2]; Ireneusz Janik[2]; Tiandi Zhuang[1]; James H. Prestegard[1]; Joshua S. Sharp[1]; *[1]University of Georgia, Athens, GA; [2]University of Notre Dame, Notre Dame, IN*

TP 509 **Structural Probing of Snap-Frozen Proteins by X-ray radiolysis and Mass Spectrometry: Radiation Damage at Work**; Sayan Gupta; Rhijuta D'Mello; Mark R. Chance; *CWRU-Center for Proteomics, Upton, NY*

TP 510 **Probing Native Structures of Homologous Large Proteins with Differential Covalent Labeling and Mass Spectrometry Characterization**; Susie Dai; Carlee Mcclintock; Robert Hettich; *Oak Ridge National Laboratory, Oak Ridge, TN*

TP 511 **A Novel Approach to Characterizing Prion Protein Structures using Chemical Labelling, Microwave-Assisted Acid Hydrolysis and MALDI-MS;** Josephine S.W. Tsang; Adina Bujold; David Wishart; Liang Li; *University of Alberta, Edmonton, Canada*

TP 512 **Extension of Fast Photochemical Oxidation of Proteins (FPOP) to Mapping Calmodulin and Calmodulin-Peptide Complexes**; Hao Zhang; Michael L. Gross; *Washington University, Saint Louis, MO*

TP 513 **Synthesis and Structural Characterization of Polyubiquitin Conjugates using High Resolution Mass Spectrometry**; Jieun Jung [1]; Marilena Manea[1]; Hans-Peter Wollscheid[2]; Martin Scheffner[2]; Michael Przybylski[1]; *[1]Laboratory of Analytical Chemistry, Konstanz, Germany; [2]Laboratory of Cellular Biochemistry, Konstanz, Germany*

TP 514 **Surface Mapping of rmetG-CSF to Determine Oligomerization Induced Difference in Surface Solvent Exposure at Neutral pH and 37 C**; Shabnam Farahmand; David M. Hambly; Himanshu S. Gadgil; Gerd R. Kleemann; Michael J. Treuheit; *Amgen, Inc., Seattle, WA*

TP 515 **Ubiquitin Conformation and Dynamics Revealed using Selective Noncovalent Adduct Protein Probing MS and Site-Directed Mutagenesis**; Zhenjiu Liu; Shijun Cheng; Daniel Gallie; Ryan R. Julian; *University of California Riverside, Riverside, CA*

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TP 549 **Differential Proteomic Analysis of C. Metalidurans Cultured under Simulated Microgravity: Application and Comparison of Three Isotope Coded Protein Labelling Strategies;** Baptiste Leroy[1]; Natalie Leys[2]; Caroline Rosier[1]; Max Mergeay[2]; Ruddy Wattiez[1]; *[1]University of Mons-Hainaut, Mons, Belgium; [2]Belgian Nuclear Research Center, Mol, Belgium*

TP 550 **Simultaneous Measurement of Protein Half-life and Precursor Pool Enrichment in *C. elegans***; Gennifer Merrihew; Michael Hoopmann; Michael J. Maccoss; *University of Washington, Seattle, WA*

TP 551 **Probing for Huntingtin Interacting Proteins using iTRAQ Technology**; Marjan Gucek; Tamara Ratovitski; Christopher A. Ross; Robert N. Cole; *Johns Hopkins School of Medicine, Baltimore, MD*

TP 552 **Effect of Hexa-carboxy Fullerenes on Differentiated Macrophages: Analysis by iTRAQ**; Timothy Sanchez[1]; Rashi Iyer[1]; Gao Jun[1]; Srinivas Iyer[1]; Sanjeev Bhardwaj[2]; James E. Carlson[3]; Shixin Sun[3]; *[1]Los Alamos National Laboratory, Los ALamos , NM; [2]Merck & Co., Inc., West Point, PA; [3]Applied Biosystems, Framingham, MA*

TP 553 **Measurement of *in vivo* Protein Turnover from Tracheal Aspirates using Targeted Proteomics**; Daniela Tomazela [1]; Michael J. Maccoss[1]; Kimberly Spencer[2]; Cole F. Sessions[2]; Elizabeth Reed[2]; Bruce Patterson[2]; Aaron Hamvas[2]; *[1]University of Washington, Seattle, WA; [2]Washington University, St Louis, MO*

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TP 555 **Survey of Estrogen-Induced Differential Protein Expression in Zebrafish Embryos using 2D-LC-MS-MS and Label-Free Relative Quantitation**; Tatjana Talamantes; Stanley M. Stevens, Jr.; Navin Rauniyar; Laszlo Prokai; *University of North Texas Health Science Center, Fort Worth, TX*

TP 556 **Quantification of Synaptosomes during Postnatal Development using 15N Labeled Rat Brain**; Daniel B. McClatchy; Lujian Liao; John R. Yates III; *The Scripps Research Institute, La Jolla, CA*

TP 557 **Spatial Mapping of the Neurite and Soma Proteomes Reveals a Functional Cdc42/Rac Regulatory Network**; Feng Yang[1]; Olivier C. Pertz[2]; yingchun wang[2]; Marina A. Gristenko[1]; Tao Liu[1]; David G. Camp II[1]; Richard L. Klemke[2]; Richard D. Smith[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]University of California, San Diego, CA*

TP 558 **Considerations in Designing Experiments for the Absolute Quantification of Proteins**; Angela K. Walker; John R. Strahler; Michael Imperiale; Philip C. Andrews; *University of Michigan, Ann Arbor, MI*

TP 559 **SILIP: A Novel Method for Stable Isotope Labeling of Proteins *in planta* for Quantitative Proteomic Analysis;** Flaubert Mbeunkui; Jennifer E. Schaff; Kevin Blackburn; David McK. Bird; Michael B. Goshe; *NC State University, Raleigh, NC*

TP 560 **Characterization and Quantification of Surfactant Proteins and Lipids in INFASURF® by Fourier Transform Ion Cyclotron Resonance Mass**

Spectrometry (FTICR); Kevin D. Quinn; Troy Wood; *University at Buffalo, Buffalo, NY*

TP 561 **Relative Quantification of Acrolein-Modified Cys-Containing Mitochondrial Peptides using MRM**; Jianyong Wu; Claudia Maier; *Oregon State University, Corvallis, OR*

TP 562 **Robust and Absolute Quantitation of PSA in Clinical Human Sera using Protein Reaction Monitoring (PRM)**; Tanguy Fortin[1]; Arnaud Salvador[2]; Jean-Philippe Charrier[1]; Christof E. Lenz[3]; Genevieve Choquet-Kastylevsky[1]; Xavier Lacoux[1]; Jerome Lemoine[2]; *[1]Biomerieux, Marcy L'etoile, France; [2]UMR 5180 Sciences Analytiques, Université Claude B, Villeurbanne, France; [3]Applied Biosystems Germany, Darmstadt, Germany*

TP 563 **Ultra Sensitive and Exact Quantification of Complex Protein Mixtures using MeCAT – Metal Coded Tagging**; Robert Ahrends[2]; Stefan Pieper[2]; Christian Scheler[1]; Michael W. Linscheid[2]; *[1]Proteome Factory AG, Berlin, Germany; [2]Humboldt-Universitaet Zu Ber, Berlin, Germany*

TP 564 **Establishing a Targeted Label-Free Protein Quantification Workflow Based on an Integrated Mass Spectrometry and Bioinformatics Platform**; Wolfgang Jabs[1]; Markus Lubeck[1]; Marina Behrens[1]; Daniel C. Chamrad[2]; Klaus Marquart[2]; Martin Blueggel[2]; Barbara Sitek[3]; Birgit Korte[3]; Sebastian Link[3]; Christian Stephan[3]; Kai Stühler[3]; Helmut E. Meyer[3]; Carsten Baessmann[1]; *[1]Bruker Daltonik GmbH, Bremen, Germany; [2]Protagen AG, Dortmund, Germany; [3]Ruhr-University Bochum, Bochum, Germany*

TP 565 **Quantitation of Protein Phosphorylation using Multiple Reaction Monitoring**; Ning Tang; Christine Miller; Keith Waddell; *Agilent Technologies, Santa Clara, CA*

TP 566 **Proteomic Analysis of the Anterior Pituitary from Long-Lived Snell Dwarf and Wild Type Mice by Q-Tof and Orbitrap FT-MS**; Jenny M. Alderman[1]; Linhong Jing[1]; Carol E. Parker [1]; Sneha Naik[1]; Natasha L. Brooks[1]; Urmila Srinivas[1]; David E. Harrison[2]; Kevin Flurkey[2]; Gunnar Boysen[1]; James A. Swenberg[1]; Xian Chen[1]; Terry P. Combs[1]; *[1]University of North Carolina, Chapel Hill, NC; [2]Jackson Laboratories, Bar Harbor, ME*

TP 567 **A Novel Strategy for Biomarker Discovery: ICPLQuant - A New Software Suite for Isotope-Labelling Based Proteomics**; Achim Brunner[1]; Eva-Maria Keidel[1]; Silke Martin[3]; Michael Kersten[2]; Josef Kellermann[1]; Friedrich Lottspeich[1]; *[1]Max Planck Institute of Biochemistry, Martinsried, Germany; [2]Toplab GmbH, Martinsried, Germany; [3]Blutspendedienst des BRK, Munich, Germany*

TP 568 **An iTRAQ-RPLC-MS-MS Approach for Protein Differential Expression Profiling of MCF7 Breast Cancer Cells: Towards Biomarker Discovery**; Jenny M. Armenta; Maria Iuliana Lazar; *Virginia Bioinformatics, Blacksburg, VA*

TP 569 **Identification and Comparative Quantitation of Protein Variants in the Ethanol-Dosed Rat Liver Mitochondrial Proteome**; Peggi M Angel[1]; Punit Shah[1]; Marshall W. Bern[3]; Marie E. Csete[2]; Ron Orlando[1]; *[1]University of Georgia, Athens, GA; [2]Emory University School of Medicine, Atlanta, GA; [3]Palo Alto Research Center, Palo Alto, CA*

TP 570 **SILAC and iTRAQ Quantitation on an Orbitrap using Protein Prospector**; Peter R Baker[2]; Xiaorong Wang[1]; Nelson Jen[1]; Lan Huang[3]; *[1]University of California,, Irvine, CA; [2]UCSF, San Francisco, CA; [3]University of California, Irvine, CA*

TP 571 **Quantitative Proteome Changes during Differentiation of Murine Erythroleukemia (MEL) Cells Assessed by SILAC Labeling and nanoLC-MS**; Gerhard Mittler; Ravi Krovvidi; *Max Planck Institute of Immunobiology, Proteomics, Freiburg, Germany*

TP 572 **Quantitative Proteomic Characterization of Colorectal and Intestinal Tumors from the *Apc^{Min}* Mouse via Metabolic Labeling**; Edward L. Huttlin[1]; Xiaodi Chen[1]; Gregory Barrett-wilt[1]; Adrian D. Hegeman[2]; Amy C. Harms[1]; William F. Dove[1]; Michael R. Sussman[1]; *[1]University of Wisconsin, Madison, WI; [2]University of Minnesota, Saint Paul, MN*

TP 573 **SILAC Reveals Heterogeneous Nuclear Ribonucleoprotein U as a Caspase Substrate in Human Colorectal Carcinoma Cells**; Fanyu Meng; Maarten Hoek; Meizhen Wu; Katie Southwick; Nathan Yates; Huseyin Mehmet; Ronald Hendrickson; *Merck & Co., Inc, Rahway, NJ*

TP 574 **Mass Spectrometry-Based Protein Localization Study to Identify New Constituents of Human Liver Peroxisomes**; Sebastian Wiese[1]; Thomas Gronemeyer[1]; Rob Ofman[2]; Martin Eisenacher[1]; Christian Stephan[1]; Heiko Hayen[3]; Ronald JA Wanders[2]; Helmut E. Meyer[1]; Bettina Warscheid[1]; *[1]Medizinisches Proteom-Center, Bochum, Germany; [2]Amsterdam Medical Center, Amsterdam, Netherlands; [3]ISAS - Institute For Analytical Sciences, Dortmund, Germany*

TP 575 **Quantitating Changes in Protein Carbonylation in Aging Rat Skeletal Muscle**; Juan Feng[1]; Hongwei Xie[2]; LaDora V Thompson[1]; Tim Griffin[1]; Edgar A. Arriaga[1]; *[1]University of Minnesota, Minneapolis, MN; [2]Waters Corporation, Milford, MA*

TP 576 **Intelligent Use of Retention Time for Higher Order Multiple Reaction Monitoring Multiplexing – Scheduled MRM**; Jose Meza; Christie L Hunter; *Applied Biosystems, Foster City,*

TP 577 **Conquering the Challenges of iTRAQ-based Relative and Absolute Quantitation of Protein Biomarkers Indicative of Dehalorespiration**; Jeffrey J Werner; Celeste Ptak; Ruth E Richardson; Sheng Zhang; *Cornell University, Ithaca, NY*

TP 578 **Comparison of Mass Spectrometry Methods for Relative Quantitative Analysis in Protein Mixtures**; John E Klimek [1]; Christine Henderson[1]; Lucinda Robertson[1]; Leif Rustvold[1]; Kerry Maddox[2]; Phillip Wilmarth[1]; Debra Mcmillen[1]; Ashok Reddy[3]; Klaus Frueh[1]; Larry David[1]; *[1]Oregon Health & Science University, Portland, OR; [2]Shriners Hospital, Portland, OR; [3]Proteogenix, Inc., Tigard, OR*

TP 579 **Development of an MRM-based Label-free Quantitative Analysis for SDS-PAGE Separated Protein Complex Samples**; Sabine Baumgart; Celeste Ptak; Amber Krauchunas; Mariana Wolfner; Sheng Zhang; *Cornell University, Ithaca, NY*

TP 580 **Stable Isotope Labeling Tandem MS (SILT) using MS2 Significantly Improves Quantitative Proteomics over Methods that Rely on Quantitation using MS1**; Kwasi G. Mawuenyega; Donald L. Elbert; Kristin R. Wildsmith; Karen R. Browning; Randall J. Bateman; *Washington University, Saint Louis, MO*

TP 581 **Relative Quantification on a Subset of the Murine Hepatic Proteome using ESI QTOF and MALDI TOF/TOF**; Richard C. Scheri; Junga Lee; Douglas F.

Barofsky; Larry R. Curtis; *Oregon State University, Corvallis, OR*

TP 582 **A Method for Rapid Differential Protein Expression Profiling from Tissue using 'Shotgun-based' LC-MS-MS and Spectral Counting**; Stanley M. Stevens, JR.; Navin Rauniyar; Vien Nguyen; Laszlo Prokai; *University of North Texas Health Science Center, Fort Worth, TX*

TP 583 **Effect of False Positive Rate and Replication Number on Identification of Proteins by UPLC-MSE**; Chongfeng Xu[1]; Thomas Neubert[2]; *[1]NYU Medical Center, New York, NY; [2]Skirball Institute, Nyumc, New York, NY*

TP 584 **Identification and Label-Free Relative Quantification of Acetylation, and Other Post-Translational Modifications using Multiple Reaction Monitoring**; Richard D Unwin; John R Griffiths; Anthony D Whetton; *University of Manchester, UK, Manchester, UK*

TP 585 **Comparison of TA-CID, HASTE CID and IRMPD for Analysis of ITRAQ & Trade; Peptides in a Quadrupole Ion Trap Mass Spectrometer**; Atim Enyenihi [1]; John R Griffiths[2]; Gary L. Glish[1]; *[1]University of North Carolina, Chapel Hill, NC; [2]Manchester University, Withington, UK*

TP 586 **Quantitative Analysis of Receptor Tyrosine Signaling in Stimulated Human Mammary Epithelial Cells**; Tyler H Heibeck[1]; Shi-jian Ding[2]; Lee Opresko[1]; Rui Zhao[1]; Athena Schepmoes[1]; David G Camp[1]; Richard D. Smith[1]; Steven Wiley[1]; Weijun Qian[1]; *[1]Pacific Northwest National Laboratory, Richland, WA; [2]University of Nebraska Medical Center, Omaha, NE*

TP 587 **Label Free Relative Quantification of Map Kinase Phosphorylation Degree by UPLC-MS**; Dominic Winter; Marcel Schilling; Ursula Klingmueller; Wolf Dieter Lehmann; *German Cancer Research Center, Heidelberg, Germany*

TP 588 **High Resolution Mass Spectrometry Proteomics Profiling of the Platelet Sheddome**; Colin G. Barry[1]; Karen P. Fong[2]; Lawrence F. Brass[2]; Ian A. Blair[1]; *[1]University of Pennsylvania, Philadephia, PA; [2]Div of Hematology Oncology Univ of Penn, Philadelphia, PA*

TP 589 **A High Sensitivity Analytical Platform for Targeted Quantitative Proteomics using Multiple Reaction Monitoring**; Tao Liu; David T. Kaleta; Errol W. Robinson; Wei-Jun Qian; Ryan T. Kelly; Jason S. Page; Keqi Tang; Heather M. Mottaz; David G. Camp II; Richard D. Smith; *Pacific Northwest National Laboratory, Richland, WA*

TP 590 **Label-Free Relative Quantification using MS-MS TIC Compared to SILAC and Spectral Counting**; John M Asara[1]; Heather Christofk[2]; Jeffrey Engelman[3]; Bin Zheng[1]; Lisa Freimark[1]; Lewis Cantley[2]; *[1]Beth Israel Deaconess Medical Center, Boston, MA; [2]Harvard Medical School, Boston, MA; [3]Massachusetts General Hospital, Boston, MA*

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TP 592 **Refinements to Proteome Quantitation Based on Spectral Counting: How to Deal with Peptides Shared by Multiple Proteins**; Zhihui Wen; Ying Zhang; Michael Washburn; Laurence Florens; *Stowers Institute for Medical Research, Kansas City, MO*

TP 593 **Quantification of Protein Expression at CEM Cells during Anti-Cancer Therapy;** Petr Pompach[1]; Petr Novak[1]; Petr Man[1]; Jan Nedved[1]; Vladimir Havlicek[1]; Petr Dzubak[2]; Marian Hajduch[2]; *[1]Institute of Microbiology, Prague 4, Czech Republic; [2]Faculty of Medicine, Palacky University, Olomouc, Czech Republic*

TP 594 **Effects of Trypsin on Spiked Isotope-labeled Tryptic Peptide Standards Used in Quantitative Proteomic Analysis**; Thomas A. Shaler[1]; Steve E. Kaiser[2]; Shanhua Lin[1]; Christopher Becker[1]; *[1]PPD Biomarker Discovery Sciences, Menlo Park, CA; [2]Stanford University, Stanford, CA*

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TP 596 **The Cisplatin-Cytochrome C Interaction Studied by Electrospray Mass Spectrometry and MSn Analysis**; Ting Zhao; Fred King; *West Virginia University, Morgantown, WV*

TP 597 **Assessing the Quality and Precision of Therapeutic Antibody LC-MS Data Acquired and Processed using Automated Workflows;** Scott Berger; Asish Chakraborty; *Waters Corporation, Milford, MA*

TP 598 **Towards More Quantitative Evaluation of PEGylated Therapeutics and Protein Aggregates by MALDI TOF MS**; Ryan Wenzel; Benoit Plet; Alexis Nazabal; *CovalX AG, Zürich, Switzerland*

TP 599 **Determining Peptide Susceptibilities to Deamidation by FTICR-MS**; Li Zhou [1]; Terry J. Amiss[2]; Carol E. Parker[1]; Xian Chen[1]; *[1]University of North Carolina - Chapel Hill, Chapel Hill, NC; [2]BD Technologies, Research Triangle Park, NC*

TP 600 **Studies Towards the Development of Milliseconds Timescale Kinetics Chips for Quantitative Monitoring of Enzyme Catalysis by MS**; Allen W. Tsang [1]; Kevin Killeen[2]; William T. Lowther[1]; Thomas J. Jönsson[1]; Cristina M. Furdui[1]; *[1]Wake Forest University School of Medicine, Winston Salem, NC; [2]Agilent Technologies, Santa Clara, CA*

TP 601 **In-gel Chemical Labeling: A Strategy for Characterization of the N-terminus and Phosphoryaltion Sites of Gel-Separated Proteins**; Joseph P Fernandez; Allison Russo; Abey Tharian; Haiteng Deng; *Proteomics Resource Center, Rockefeller University, New York, NY*

TP 602 **Beta-Elimination of Disulfide Bridges: A Common Sample Preparation Induced Protein Modification**; Tomas Rejtar; Christian Baumgartner; Majlinda Kullolli; Barry L. Karger; *Northeastern University, Boston, MA*

TP 603 **LC-MS and LC-MS-MS Characterization of CMC-544: A CD22-Targeted Immunoconjugate of Calicheamicin**; Jason X. Tang; Eugene Vidunas; Fang (anna) Wang; Justin Moran; *Wyeth Research, Pearl River, NY*

TP 604 **Gas-Phase Ion/Ion Chemistry and Mass Spectrometry for the Determination of Alpha-1-Anti Trypsin Inhibitor Oxidation Sites**; Harsha P. Gunawardena; *Talecris Biotherapeutics, Research Triangle Park, NC*

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TP 605 **An Alternative Peptide Precursor Ion Selection Strategy for Protein Identification by Mass Spectrometry**; David A. Barnett; Rodney J. Ouellette; *Atlantic Cancer Research Institute, Moncton, Canada*

TP 606 **A New Approach to Achieving a Fast, In-depth Biological Overview of MS-Based Proteomics Data**; Christian Ravnsborg Ingrell; Martin Damsbo; Peter Venø; Morten Bern; *Proxeon A/S, Odense, Denmark*

TP 607 **Complementary Mass Spectrometry or Just Questionable Identifications?**; Scott Geromanos; *Waters Corporation, Milford, MA*

TP 608 **High Resolution Analysis of the Human Proteome by Middle down Mass Spectrometry: A LC-FT-ICR-MS-MS Platform Bringing Sanity to Proteomics**; Michael T. Boyne II; Mingxi Li; Cong Wu; Leonid Zamdborg; Shannee Babai; Neil L. Kelleher; *University of Illinois, Urbana-Champaign, IL*

TP 609 **The PeptideAtlas as a Tool for Targeted Proteomics**; David S Campbell[1]; Eric Deutsch[2]; Vinzenz Lange[3]; Paola Picotti[4]; Nichole King[2]; Simon Letarte[2]; Henry Lam[2]; Ning Zhang[2]; Ruedi Aebersold[5]; *[1]ISB, Seattle, WA; [2]Institute For Systems Biology, Seattle, WA; [3]3m, Ham Lake, MN; [4]Institute For Molecular Systems Biology, Zuerich, Switzerland; [5]Swiss Federal Institute of Technology, Zurich, Switzerland*

TP 610 **Single-Hit and Biochemical Pathway Directed Proteomic Profiling**; Brook L. Nunn[1]; Shawna Hengel[1]; Theodore Larson Freeman[1]; Soyoung Ryu[1]; Eric J. Foss[2]; David R. Goodlett[1]; *[1]University of Washington, Seattle, WA; [2]University of Washington and Fred Hutchinson Cancer Center, Seattle, WA*

TP 611 **Intelligent Data Annotation Workflows Applied to the Characterization of Human Cerebrospinal Fluid**; Roger G. Biringer[1]; Zhiqi Hao[1]; Helen Tran[1]; Michael G. Harrington[2]; Andreas F. R. Hühmer[1]; *[1]Thermo Fisher Scientific, San Jose, CA; [2]Huntington Medical Research Institutes, Pasadena, CA*

TP 612 **Cross-Sample and Cross-Platform Training of Peptide Detectability**; Randy J. Arnold; Yong F. Li; Predrag Radivojac; Haixu Tang; *Indiana University, Bloomington, IN*

TP 613 **SMART-Directed LC-MALDI Protein Identification using a MALDI-Ion Trap-TOF Mass Spectrometer**; Matthew E. Openshaw[1]; Rachel L. Martin[1]; John M. Allison[2]; Victor Spicer[3]; Werner Ens[3]; Oleg V. Krokhin[3]; *[1]Shimadzu Biotech, Manchester, UK; [2]Kratos Analytical Ltd., Manchester, UK; [3]University of Manitoba, Winnipeg, Canada*

TP 614 **Mining in a MudPIT: Digging Deeper with PLGEM**; S Swanson; N Pavelka; L Florens; M Washburn; *Stowers Institute For Medical Research, Kansas City, MO*

TP 615 **Targeted Peptide Identification Based on Selected Reaction Monitoring**; Bruno Domon; Paola Picotti; Nathalie Selevsek; Ruedi Aebersold; *IMSB - ETH Zurich, Zurich, Switzerland*

TP 616 **Efficient Mining by Optimizing Acquisition Time and Sample Consumption: MALDI-TOF MS-MS Analysis of Low and High Complexity Protein Digests**; Patrick Pribil; Aaron Booy; Suzanne Ackloo; Gordana Ivosev; Min J. Yang; *MDS Sciex, Concord, ON*

TP 617 **Determining Unassignable Peptides in Accurate Mass Measurement Shotgun Proteomics**; Chunyan Li; Melissa Warren; William B. Whitman; Jon Amster; Yuchen liu; *University of Georgia, Athens, GA*

TP 618 **A Bayesian Approach for Addressing the Protein Inference Problem in Shotgun Proteomics**; Yong F. Li; Randy J. Arnold; Predrag Radivojac; Haixu Tang; *Indiana University, Bloomington, IN*

TP 619 **Iterative MS-MS Sampling of Proteomics Mixtures: Software and Methodology to Maximize Sampling of Detectable Components in Mixture**; Michael R. Hoopmann; Daniela Tomazela; Michael J. Maccoss; *University of Washington, Seattle, WA*

TP 620 **Posterior Peptide Identification for Proteomics Data Analysis**; Haixu Tang; Yong F. Li; Randy J. Arnold; Predrag Radivojac; *Indiana University, Bloomington, IN*

TP 621 **Duty Cycle and MRM Prediction Improvements for Protein ID Validation using the MIDAS Workflow on a QqLIT Mass Spectrometer**; Christof E. Lenz [1]; Henning Urlaub[2]; Matthias Glueckmann[1]; *[1]Applied Biosystems, Darmstadt, Germany; [2]Max Planck Institute, Goettingen, Germany*

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TP 622 **Discovery of Wound Healing Markers: MALDI-MS Methodology for Wound Fluid Analysis and In Situ Imaging of Formalin-Fixed Paraffin Embedded Tissues**; Katri Huikko; Stephanie F Bernatchez; Patrick J Parks; Bathsheba Chong Conklin; *3M, St Paul, MN*

TP 623 **The Application of MALDI-TOF MS Plasma Protein Profiling for Discrimination of Patients with Squamous Cell Carcinomas from Healthy Controls**; Valeriy E. Shevchenko; Natalia E. Arnotskaya; Sergei S. Aushkap; Valentina A. Yurchenko; David G. Zaridze; *N. N. Blokhin Russian Cancer Research Center, Moscow, Russia*

TP 624 **Biomarker Discovery Of Amniotic Fluid From Patients with Posterior Urethral Valve Syndrome using Proteomics Strategies**; Jenny Albanese[3]; Olga Miroshnychenko[2]; H. Eva Witkowska[2]; Haichuan Liu[2]; Hanmin Lee[1]; Marjorie Minkoff[3]; Susan Fisher[2]; Raul Cortes[1]; *[1]UC San Francisco Fetal Treatment Center, San Francisco, CA; [2]Department of Cell and Tissue Biology, San Francisco, CA; [3]Applied Biosystems in Foster City, San Francisco, CA*

TP 625 **A Non-Parametric Statistical Method to Assess Humoral Response in Pancreatic Cancer**; Tasneem H. Patwa; Huy Vuong; Laila Poisson; Debashis Ghosh; David E. Misek; Diane M. Simeone; David M. Lubman; *University of Michigan, Ann Arbor, MI*

TP 626 **Detection of Tumor-Derived Peptides in Pancreas Cancer Patient Plasma**; Kwasi Antwi; *The Biodesign Institute, Arizona State University, Tempe, AZ*

TP 627 **LC-MS(E) Analysis of Human Urine Proteome**; Martin Gilar; Petra Olivova; Scott Geromanos; John Gebler; *Waters Corporation, Milford, MA*

TP 628 **Proteomic Analysis of Membrane Glycoproteins using a Lectin Affinity Approach**; Yanfei Wang; Huy Vuong; David M. Lubman; *University of Michigan, Ann Arbor, MI*

TP 629 **Proteomic Markers in Prostate Tissue by Histology Directed Profiling Mass Spectrometry and LC-MS(MS)2, Malignant Vs. Adjacent Benign Tissue Sections**; Sean Clark; Jared Cox; Donald Shipman; Colleen Martin; Greg Bowersock; Christopher Amling; James Mobley; *University of Alabama at Birmingham, Birmingham, AL*

TP 630 **Enhanced Biomarker Discovery using Pathway Markers, Density Based Fractionation and MALDI-**

MS-MS; WenKui Lan; Marc Horn; *Prospect Biosystems, LLC, Newark, NJ*

TP 631 **Programmable Proteomics for High Throughput Validation of Salivary Oral Cancer Protein Biomarkers**; Ebbing de Jong[1]; Hongwei Xie[2]; Getiria Onsongo[1]; John V Carlis[1]; Nelson L Rhodus[1]; Frank G Ondrey[1]; Tim Griffin[1]; *[1]University of Minnesota, Minneapolis, MN; [2]Waters Corporation, Milford, MA*

TP 632 **Comparison Proteome Analysis of Two Closely-Related Ovarian Endometrioid Adnocarcinoma(OEA)-Derived Cell Lines**; Lan Dai; David M. Lubman; *University of Michigan, Ann Arbor, MI*

TP 633 **Discovery of O-linked Glycoprotein Cancer Biomarkers in Human Sera by Multi-Lectin Enrichment and Lectin Microarray Binding Patterns with MALDI QIT**; Chen Li[1]; David M Lubman[1]; Fan Xiang[2]; *[1]University of Michigan, Ann Arbor, MI; [2]Shimadzu, Pleasanton, Ca*

TP 634 **Identification of 4-Hydroxynonenal Targets in Plasma Proteins using Click Chemistry**; Hye-Young H. Kim; Simona G. Codreanu; Keri A. Tallman; Ned A. Porter; Daniel C. Liebler; *Vanderbilt University, Nashville, TN*

TP 635 **Identifying Candidate Protein Markers for Colorectal Cancer from Human Stool**; Patrick S. Quint; Douglas W. Mahoney; Ann L. Oberg; Garth D. Nelson; Jonathan J. Harrington; David A. Ahlquist; H. Robert Bergen, III; *Mayo Clinic College of Medicine, Rochester, MN*

TP 636 **Pancreatic Cancer Biomarkers: Post-Translational State of Nuclear and Cytosolic High Mobility Group Box Protein-1 [HMGB1] as Determined by MALDI-TOF MS**; L.J. Sparvero [1]; Shelly A. Kucherer[2]; Herbert J. Zeh[1]; Michael T. Lotze[1]; Andrew A. Amoscato[1]; *[1]University of Pittsburgh, Pittsburgh, PA; [2]Carnegie Mellon University, Pittsburgh, PA*

TP 637 **Proteomic Approaches for Detection of Metabolic Syndrome in Obese Adults**; Jacob A. Galan; Corrie Whisner; Stacy L. Mobely; W. Andy Tao; *Purdue University, West Lafayette, IN*

TP 638 **Discovery of Pancreatic Cancer Biomarker for Early Detection: Proteomic Analysis of Human Pancreatic Duct Fluid (Juice)**; Vadiraja B. Bhat; Lei Shi; Christopher Thompson; Rebecca Wiatrek; Mohsen Shabahang; Arundhati Rao; Alexzander A. Asea; *Scott & White Memorial Hospital, Temple, TX*

TP 639 **Discovery of Schizophrenia Biomarker Proteins in Eccrine Sweat**; Mark M. Ross[1]; Michelle Raiszadeh[1]; Weidong Zhou[1]; Emanuel Petricoin[1]; Lance Liotta[1]; April Dickson[2]; Cindy Dickson[2]; Adam Freeberg[2]; Mary Ann Schaepper[2]; Wolff Kirsch[2]; *[1]George Mason University, Manassas, VA; [2]Loma Linda University, Loma Linda, CA*

TP 640 **Comparative Proteomics of Human Intraductal Carcinoma and Matched Normal Breast Tissues: Biomarkers and Insights into Molecular Basis of DCIS Development**; Lambert C. Ngoka; *Virginia Commonwealth Univ., Richmond, VA*

TP 641 **Nonporous Silica Reverse-Phase High-Performance Liquid Chromatography -Electrospray Tandem Mass Spectrometry (NPS-HPLC-ESI-MS-MS) with ExacTag Labeling for Lung Cancer Plasma Protein Characterization**; Karan Bedi[3]; Xiaoping Ao[2]; Fengming Kong[2]; David M. Lubman[1]; *[1]University of Michigan, Ann Arbor, MI; [2]University of Michigan Medical Center, Ann Arbor, MI; [3]School of Public Health, University of Michigan, Ann Arbor, MI*

TP 642 **Quantitative Analysis of the Malignant Glioma Secretome**; Catherine Formolo; Tobey J MacDonald; Yetrib Hathout; *Children's National Medical Center, Washington, DC*

TP 643 **Differential Proteomics of Secreted Proteins for Melanoma Biomarker Discovery**; Mathur Rajesh; Lalita A. Shevde; Rajeev S. Samant; Adam I. Riker; Lewis K. Pannell; *Mitchell Cancer Institute, Mobile, AL*

TP 644 **Site-Specific Identification of Protein Markers of Organophosphorus Compounds Exposure using Monomeric Avidin Purification**; Shi-Jian Ding[1]; Bin Li[1]; John Carr[2]; Larry Schopfer[1]; Steven Hinrichs[1]; Oksana Lockridge[1]; *[1]University of Nebraska Medical Center, Omaha, NE; [2]Missouri Southern State University, Joplin, MO*

TP 645 **Biomarker Discovery using Low Enrichment Stable Isotope Labeling of Amino Acids in Cells**; Jing Xiao[1]; Wai-Nang Paul Lee[2]; Shu Lim[2]; Yingchun Zhao[1]; Robert Recker[1]; Gary Guishan XIAO[1]; *[1]Creighton University Medical Center, Omaha, NE; [2]Mass Spectrometry Core Facility, Pediatrics, Los Angeles, California*

TP 646 **Biomarker Discovery by Stable Isotope Labeling and Quantitative Mass Spectrometry in a Trait Anxiety Mouse Model**; Christoph W. Turck; Katrin Haegler; Elisabeth Frank; Melanie Kessler; Boris Hambsch; Yuji Odagaki; Birgit Bisle; Rainer Landgraf; Christian Webhofer; *Max Planck Institute of Psychiatry, Munich, Germany*

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TP 647 **A Program to Statistically Evaluate Mass Spectra for Identification of Differentiating Features and Biomarker Discovery**; Sean Beecroft[1]; Scott Kronewitter[1]; Maria Lorna A de Leoz[1]; Nannan Tao[1]; Suzanne Miyamoto[2]; Ruth Vinall[2]; Ralph deVere White[2]; Kit Lam[2]; Hyun Joo An[1]; Carlito Lebrilla[1]; *[1]University of California, Davis, CA; [2]UC Davis Cancer Center, Sacramento, CA*

TP 648 **Multi-Spectra Peptide Sequencing and its Applications to Multistage Mass Spectrometry**; Nuno Bandeira[1]; Jesper V Olsen[2]; Matthias Mann[2]; Pavel Pevzner[1]; *[1]University of California, San Diego (UCSD), La Jolla, CA; [2]Max Planck Institute For Biochemistry, D Martinsried, Germany*

TP 649 **The MCW Automated Proteomics Workflow (MAPW)**; Brian D. Halligan; Andrew Vallejos; Simon Twigger; Andrew Greene; *Medical College Of Wisconsin, Milwaukee, WI*

TP 650 **Absolute Protein Quantification Estimated by Spectral Counting using Large Datasets in PeptideAtlas**; Ning Zhang[1]; Eric Deutsch[1]; Henry Lam[1]; Ruedi Aebersold[2]; *[1]Institute for Systems Biology, Seattle, WA; [2]Swiss Federal Institute of Technology, Zurich, Switzerland*

TP 651 **Spectral Clustering of MS-MS Data to Identify Unknown Peptide Modifications and Estimate Identifiable Spectra**; Jayson A Falkner; Anastasia K Yocum; Pratik D Jagtap; Philip C Andrews; *University of Michigan, Ann Arbor, MI*

TP 652 **Chemical Contaminants in Proteomics LC-MS Data**; Xinjian Yan; Stephen Stein; *NIST, Gaithersburg, MD*

TP 653 **Better Protein Quantification by Combining Peptide Identification Confidence and Retention-Time Prediction**; Lei Xin[1]; Weiwu Chen[2]; Weijie Yang[2]; Sean

Bendall[1]; BIN MA[1]; Gilles Lajoie[1]; [1]*University of Western Ontario, London, ON, Canada;* [2]*Bioinformatics Solutions Inc., Waterloo, ON, Canada*

TP 654 **Planets, Proteins, and Portability: A Common API and Desktop Environment for Proteomics Data Analysis**; Manor Askenazi [1]; Jignesh Parikh[2]; Tanya Cashorali[3]; Yi Zhang[2]; Scott Ficarro[2]; Nathaniel C. Blank[4]; Jarrod Marto[2]; [1]*Dana-Farber Cancer Institute and Hebrew University, Boston, MA;* [2]*Dana-Farber Cancer Institute, Boston, MA;* [3]*Northeastern University, Boston, MA;* [4]*Centre College, Danville, KY*

TP 655 **A Public Network for Publishing Proteomics Data and Tools**; Philip C Andrews; Bryan E Smith; James A Hill; Mark A Gjukich; Jayson A Falkner; *University of Michigan, Ann Arbor, MI*

TP 656 **Two-phase Filtering Strategy for Identification of Peptide with Post-Translational Modifications**; Kang Ning[1]; Xia Cao[1]; Hoong Kee Ng[2]; Hon Wai Leong[2]; Alexey I. Nesvizhskii[1]; [1]*University of Michigan, Ann Arbor, MI;* [2]*National University of Singapore*

TP 657 **Molecular Fragmentation Query Language for Shotgun Lipidomics**; Ronny Herzog; Dominik Schwudke; Andrej Shevchenko; *Max Planck Institute CBG, Dresden, Germany*

TP 658 **Automated Evaluation of Peptide Identifications from Shotgun Proteomics Data by Use of Peptide Hydrophobicity and Reversed-Phase LC Retention Time**; Hua Xu; Lanhao Yang; Michael A. Freitas; *Ohio State University, Columbus, OH*

TP 659 **AB3D: A Suite of Algorithms for Biomarker Discovery in Diagnostics and Drug Development using LC-MS**; Ken Aoshima[1]; Satoshi Tanaka[2]; Yuji Miura[1]; Yoshiya Oda[1]; Tatsuji Nakamura[1]; Hiromi Ohashi[1]; Masataka Ueda[1]; Akiyoshi Suganuma[1]; Junro Kuromitsu[1]; [1]*Eisai Co., Ltd, Tsukuba, Japan;* [2]*CREST, Japan Science and Technology, Saitama, Japan*

TP 660 **Evaluating Efficiency of Cross-Species Comparisons**; A. Podtelejnikov; D. Potter; C. R. Ingrell; S. Larsen; *Proxeon A/S, Odense, Denmark*

TP 661 **Mascot Percolator: Improved Peptide and Protein Identification**; Markus Brosch; Tim Hubbard; Jyoti Choudhary; *Wellcome Trust Sanger Institute, Cambridge, UK*

TP 662 **How Stable are Peptide Identifications with Regards to Variations in MS-MS Spectra?**; Pierre-Alain Binz[1,2]; Markus Müller[2]; Frederique Lisacek[2]; David Bouyssié[3]; [1]*Genebio, Geneva, Switzerland;* [2]*Swiss Institute of Bioinformatics, Geneva, Switzerland;* [3]*IPBS, Toulouse, France*

TP 663 **Methods to Estimate the Precision of False Positive Rate Measured by Decoy Protein Database Searching**; Roger Moore; Mary K. Young; Terry Lee; *City of Hope, Duarte, CA*

TP 664 **Alternative Splicing Database for Bottom-up and Top-down Protein Identification**; Kung-Yen Chang; D. Ryan Georgianna; Steffen Heber; Gary A. Payne; David C. Muddiman; *North Carolina State University, Raleigh, NC*

TP 665 **ABRF iPRG 2008 Study: Characterization of Protein Inference Reporting from Proteomics Studies**; Brian C. Searle[1]; David L. Tabb[2]; Alexey I. Nesvizhskii[3]; William S. Lane[4]; Jeffery A. Kowalak[5]; Jayson A. Falkner[3]; Sean L. Seymour[6]; [1]*Proteome Software, Portland, OR;* [2]*Vanderbilt University Medical Center, Nashville, TN;* [3]*University of Michigan, Ann Arbor, MI;* [4]*Harvard University, Cambridge, MA;* [5]*National Institute of Mental Health, Bethesda, MD;* [6]*Applied Biosystems, Foster City, CA*

TP 666 **Monte Carlo Simulation Based Algorithms for Scoring Ion Abundance and Peptide Sequence Tags in Database Searches of Shotgun-Proteomic Data**; Michael A. Freitas; Hua Xu; *Ohio State University, Columbus, OH*

TP 667 **Identification of Peptides from Data-Independent Tandem MS**; Marshall W. Bern[1]; Gregory Finney[2]; Michael J. Maccoss[3]; Michael Hoopmann[3]; [1]*Palo Alto Research Center, Palo Alto, CA;* [2]*Univ of Washington, Genome S, Seattle, WA;* [3]*University of Washington, Seattle, WA*

TP 668 **iProphet: A New Tool for Combining PeptideProphet Results from Multiple Search Engines Improves Spectrum Validation**; David Shteynberg[1]; Alexey Nesvizhskii[2]; Eric Deutsch[1]; Henry Lam[1]; Ruedi Aebersold[3]; [1]*Institute for Systems Biolog, Seattle, WA;* [2]*University of Michigan, Ann Arbor, MI;* [3]*Swiss Federal Institute of Technology, Zurich, Switzerland*

TP 669 **New Developments for Open-Source Shotgun Proteomics Analysis with the Trans-Proteomic Pipeline**; Joshua Tasman[1]; Luis Mendoza[1]; David Shteynberg[1]; James Eddes[1]; Ning Zhang[1]; Chee-Hong Wong[3]; Brian S Pratt[2]; Henry Lam[1]; Jimmy Eng[4]; Eric Deutsch[1]; Ruedi Aebersold[5]; [1]*Institute for Systems Biology, Seattle, WA;* [2]*Insilicos Llc, Seattle, WA;* [3]*Bioinformatics Institute, Singapore, Singapore;* [4]*University of Washington, Seattle, WA;* [5]*Swiss Federal Institute of Technology, Zurich, Switzerland*

TP 670 **Rapid Cyberinfrastructure Evolution for Proteomics Research**; Claudiu Farcas; To-ju Huang; Sam Payne; Nuno Bandeira; Ari Frank; Nitin Gupta; Pavel Pevzner; Ingolf Krueger; Vineet Bafna; *UCSD, La Jolla, CA*

TP 671 **Empirical Evaluation of Algorithm Consensus Methods to Peptide Identification**; Tamanna Sultana; Rick Jordan; James Lyons-Weiler; *University of Pittsburgh, Pittsburgh, PA*

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TP 672 **Interpretation of Proteomic 2D Electrophoresis and MALDI TOF/TOF Data using Pathway Analysis Tools to Understand Muscle Development**; Matthew Mcdonagh; Matthew Knight; *Biosciences Research Division, DPI Victoria, Melbourne, Australia*

TP 673 **Comprehensive Analysis of Murine Adipose Tissue by Detergent-Free Pressure Cycling Protein Extraction and High Resolution Tandem Mass Spectrometry**; Emily Freeman[1]; Vera Gross[2]; Gary Smejkal[2]; Alexander Lazarev[2]; Haiming Cao[1]; Gokhan S. Hotamisligil[1]; Alexander R. Ivanov [1]; [1]*Harvard University, Boston, MA;* [2]*Pressure Biosciences, Inc, Woburn, MA*

TP 674 **Mapping the Entamoeba Histolytica Proteome using Subcellular Fractionation, One-Dimensional Polyacrylamide Gel Electrophoresis and Liquid Chromatography-Tandem Mass Spectrometry**; Barbora Maralikova; Jorge Tovar; *Royal Holloway University of London, Egham, Surrey*

TP 675 **Novel Insights into Platelet Biochemical Processes by a Combination of Unbiased, Comprehensive Proteomic Analysis by Mass Spectrometry and Pathway Analysis**; Geraldine M Walsh; Michael D Hoffman; Dana V Devine; Ronald C. Beavis; Juergen Kast; *University of British Columbia, Vancouver, Canada*

TUESDAY POSTERS

TP 676 **The Study of *Botrytis cinerea* Interaction with Tomatoes**; Punit Shah[1]; Gerardo Gutierrez-sanchez[2]; James A Atwood Iii[2]; Ann Powell[3]; Ron Orlando[2]; Carl Bergmann[1]; *[1]Complex Carbohydarate Research Center, Athens, GA; [2]University of Georgia, Athens, GA; [3]University of California, Davis, California*

TP 677 **Proteogenome Profiling of Acholeplasma Laidlawii;** Vadim Govorun; *Institute of Physico-Chemical Medicine, Moscow, Russian Federation*

TP 678 **The Human Saliva Proteome: Collection, Stability, and Analysis**; Timothy Britt Langston; Rebecca R. Secrist; Gaurav S.J.B. Rana; Michael J. Oldham; Jason W. Flora; *Philip Morris USA, Richmond, VA*

TP 679 **The Secretomes on the Interface of *Magnaporthe grisea*-Rice Leaf Interaction**; Gerardo Gutierrez-Sanchez; Punit Shah; James A Atwood III; Denise Lennon; Peter Albersheim; Alan Darvill; Ron Orlando; Sheng-Cheng Wu; *Complex Carbohydarate Research Center, Athens, GA*

TP 680 **Gauging Complementary Proteomics Discovery of *Nostoc punctiforme* PCC 73102 using a Combination of FFE, SCX, Ion-Trap and QTOF-MS**; Saw Yen Ow[1]; Nishikant Wase[1]; Mikkel Nissum[2]; Phillip C Wright[1]; *[1]University of Sheffield, Sheffield, UK; [2]BD Diagnostics, Martinsried, Germany*

TP 681 **Processing of High Mass Accuracy MS-Data from Large-Scale Proteomics Experiments and Construction of Proteotypic Library for the Arabidopsis Thaliana Proteome**; Boris Zybailov; Giulia Friso; Paul Dominic B. Olinares; Heidi Rutschow; Klaas van Wijk; Qi Sun; *Cornell University, Ithaca, NY*

TP 682 **Identification of Cancer Specific Protein Classes using Non-Tagged Proteomics Combined with Systems Biology Applied to Murine Models of Breast Cancer**; Anton Poliakov; Yuelong Liu; Gregory Bowersock; Huang-Ge Zhang; James Mobley; *University of Alabama at Birmingham, Birmingham, AL*

TP 683 **Deciphering Pluripotency of Embryonic Stem Cells through Transcriptome, Proteome and Modificome**; Rong Zeng; Qing-Run Li; Jiu-Hong Kang; Jie Dai; Xiao-Bin Xing; Yi-Xue Li; *Shanghai Institutes for Biological Sciences, Shanghai, China*